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(54) Title: CELL-WALL DEGRADING ENZYME VARIANTS

(57) Abstract: A variant of a cell-wall degrading enzyme having a beta-helix structure, which variant holds at least one substituent in a position determined by identifying all residues potentially belonging to a stack; characterising the stack as interior or exterior; characterising the stack as polar, hydrophobic or aromatic/heteroaromatic based on the dominating characteristics of the parent or wild-type enzyme stack residues and/or its orientation relative to the beta-helix (interior or exterior); optimising all stack positions of a stack either to hydrophobic aliphatic amino acids, hydrophobic aromatic or polar amino acids by allowing mutations within one or all positions to amino acids belonging to one of these groups; measuring thermostability of the variants by DSC or an application-related assay such as a Pad-Steam application test; and selecting the stabilized variants. Variant of a wild-type parent pectate lyase (EC 4.2.2.2) having the conserved amino acid residues D111, D141 or E141, D145, K165, R194 and R199 when aligned with the pectate lyase comprising the amino acid sequence of SEQ ID NO: 2 are preferred.

CELL-WALL DEGRADING ENZYME VARIANTS

The present invention relates to variants of microbial cell-wall degrading enzymes, more specifically to variants of enzymes having a pectinase structure similar to that of *Bacillus licheniformis* enzymes exhibiting pectate lyase activity as their major enzymatic activity in the neutral and alkaline pH ranges; to a method of producing such enzymes; and to methods for using such enzymes in the textile, detergent and cellulose fiber processing industries. The enzyme variants of the invention may exhibit increased thermostability as compared to the parent enzyme.

BACKGROUND OF THE INVENTION

Plant cell walls consist of a complicated network of fibrous materials. The composition of the cell walls varies considerably, depending on the source of the vegetable material. However, in general its composition can be summarized as mainly comprising non-starch polysaccharides. These polysaccharides can be found in various forms: cellulose, hemicellulose and pectins.

The composition of a plant cell wall is both complex and variable. Polysaccharides are mainly found in the form of long chains of cellulose (the main structural component of the plant cell wall), hemicellulose (comprising e.g. various .beta.-xylan chains) and pectin. The occurrence, distribution and structural features of plant cell wall polysaccharides are determined by: 1. Plant species; 2. Variety; 3. Tissue type; 4. Growth conditions; and 5. Ageing (Chesson (1987), Recent Advances in Animal Food Nutrition, Haresign on Cole, eds.). Butterworth, London, 71-89).

Basic differences exist between monocotyledons (e.g. cereals and grasses) and dicotyledons (e.g. clover, rapeseed and soybean) and between the seed and vegetative parts of the plant (Carre' and Brillouet (1986), Science and Food Agric. 37, 341-351). Monocotyledons are characterized by the presence of an arabinoxylan complex as the major hemicellulose backbone. The main structure of hemicellulose in dicotyledons is a

xyloglucan complex. Moreover, higher pectin concentrations are found in dicotyledons than in monocotyledons. Seeds are generally very high in pectic substances, but relatively low in cellulosic material. Three more or less interacting polysaccharide structures can be distinguished in the cell wall:

1. The middle lamella forms the exterior cell wall. It also serves as the point of attachment for the individual cells to one another within the plant tissue matrix. The middle lamella consists primarily of calcium salts of highly esterified pectins;

2. The primary wall is situated just inside the middle lamella. It is a well-organized structure of cellulose microfibrils embedded in an amorphous matrix of pectin, hemicellulose, phenolic esters and proteins;

3. The secondary wall is formed as the plant matures.

During the plant's growth and ageing phase, cellulose microfibrils, hemicellulose and lignin are deposited.

There is a high degree of interaction between cellulose, hemicellulose and pectin in the cell wall. The enzymatic degradation of these rather intensively cross-linked polysaccharide structures is not a simple process. A large number of enzymes are known to be involved in the degradation of plant cell walls. They can broadly be subdivided in cellulases, hemicellulases and pectinases (Ward and Young (1989), CRC Critical Rev. in Biotech. 8, 237-274).

Cellulose is the major polysaccharide component of plant cell walls. It consists of .beta. 1,4 linked glucose polymers.

Cellulose can be broken down by cellulases, also called cellulolytic enzymes. Cellulolytic enzymes have been divided traditionally into three classes: endoglucanases, exoglucanases or cellobichydrolases and .beta.-glucosidases (Knowles, J., et al. (1987), TIBTECH 5, 255-261). Like all cell wall degrading enzymes they can be produced by a large number of bacteria, yeasts and fungi. Apart from cellulases degrading .beta.-1,4 glucose polymers, endo-1,3/1,4 .beta.-glucanases and xyloglucanases should be mentioned (Ward and Young op. cit.).

Pectins are major constituents of the cell walls of edible

parts of fruits and vegetables. The middle lamella which are situated between the cell walls are mainly built up from protopectin which is the insoluble form of pectin. Pectins are considered as intracellular adhesives and due to their colloidal nature they also have an important function in the water regulation system of plants. The amount of pectin can be very high. For example, lemon peels are reported to contain pectin at up to 30% of their dry weight, orange peels contain from 15-20% and apple peels about 10% (Norz, K. (1985). Zucker und Susswaren Wirtschaft 38, 5-6).

Pectins are composed of a rhamno-galacturonan backbone in which 1,4- linked (.alpha.-D-galacturonan chains are interrupted at intervals by the insertion of 1,2-linked (.alpha.-L-rhamnopyranosyl residues (Pilnik, W. and A. Voragen (1970), In: The Biochemistry of fruits and their products, vol. 1, Chapter 3, p. 53. Acad. Press). Other sugars, such as D-galactose, L-arabinose and D-xylose, are present as side chains. A large part of the galacturonan residues is esterified with methyl groups at the C2 and C3 position.

A large number of enzymes are known to degrade pectins. Examples of such enzymes are pectin esterase, pectin lyase (also called pectin transeliminase), pectate lyase, and endo- or exo-polygalacturonase (Pilnik and Voragen (1990). Food Biotech 4, 319-328). Apart from enzymes degrading smooth regions, enzymes degrading hairy regions such as rhamnogalacturonase and accesory enzymes have also been found (Schols et al. (1990), Carbohydrate Res. 206, 105-115; Searle Van Leeuwen et al. (1992). Appl. Microbiol. Biotechn. 38, 347-349).

Pectinases can be classified according to their preferential substrate, highly methyl-esterified pectin or low methyl-esterified pectin and polygalacturonic acid (pectate), and their reaction mechanism, beta-elimination or hydrolysis. Pectinases can be mainly endo-acting, cutting the polymer at random sites within the chain to give a mixture of oligomers, or they may be exo-acting, attacking from one end of the polymer and producing monomers or dimers. Several pectinase activities acting on the smooth regions of pectin are included

in the classification of enzymes provided by the Enzyme Nomenclature (1992) such as pectate lyase (EC 4.2.2.2), pectin lyase (EC 4.2.2.10), polygalacturonase (EC 3.2.1.15), exo-polygalacturonase (EC 3.2.1.67), exo-polygalacturonate lyase (EC 4.2.2.9) and exo-poly-alpha-galacturonosidase (EC 3.2.1.82).

Pectate lyases degrade un-methylated (polygalacturonate) or low-methylated pectin by β-elimination of the α-1,4-glycosidic bond. The enzymes are generally characterised by an alkaline pH optimum, an absolute requirement for Ca^{2+} (though its role in binding and catalysis is unknown) and good temperature stability.

Pectate lyases have been cloned from different bacterial genera such as *Bacillus*, *Erwinia*, *Pseudomonas*, *Klebsiella* and *Xanthomonas*.

US Patent Application Serial No. 09/073,684, which is hereby incorporated by reference in its entirety, discloses a cloned *Bacillus licheniformis* pectate lyase. The DNA sequence encoding this *B.licheniformis* pectate lyase and the deduced amino acid sequence are listed in the appended sequence listing as SEQ ID NOS. 1 and 2, respectively.

The crystal structures of pectate lyases of *Bacillus subtilis* (1BN8[1] (and an R279K mutant, 2BSP[2])), of *Erwinia chrysanthemi* (PelC: 2PEC[3]/1AIR[4]; PelC (R218K) in complex with substrate: ref 10; and PelE: 1PCL[5]), of *Erwinia carotovora* (PelC: 1PLU[6]), and of *Bacillus sp.* strain 2 KSM-P15 (1EE6) have been published. In addition, the crystal structures of the structurally very similar pectin lyases from *Aspergillus niger* (PlyA:1IDJ[7]/1IDK[7] and PlyB:1QCX[8]) and of the polygalacturonase from *Erwinia carotovora* (1BHE[9]) are also known (1: R. Pickersgill, J. Jenkins, G. Harris, W. Nasser, J. Robert-Baudrouy; *Nat.Struct.Biol.* **1994**, *1*, 717;

2: R. Pickersgill, K. Worboys, M. Scott, N. Cummings, A. Cooper, J. Jenkins, D. Smith To Be Published;

3: M. D. Yoder, S. E. Lietzke, F. Jurnak; *Structure* , 1993, *1*, 241;

4: M. D. Yoder, N. T. Keen, F. Jurnak; *Science*, **1993**, *260*, 1503;

5: M. D. Yoder, C. A. Dechaine, F. Jurnak; *J.Biol.Chem.* **1990**, *265*, 11429;

6: S. J. Tamaki, S. Gold, M. Robeson, S. Manulis, N. T. Keen; *J.Bacteriol.* **1988**, *170*, 3468;

7: S. E. Lietzke, R. D. Scavetta, M. D. Yoder, F. A. Jurnak; *Plant Physiol.* **1996**, *111*, 73;

8: S. E. Lietzke, N. T. Keen, F. Jurnak; To Be Published;

9: Y. Kim, V. Mosser, N. Keen, F. Jurnak; *J.Mol.Biol.* **1989**, *208*, 365; N. T. Keen, S. Tamaki; *J.Bacteriol.* **1986**, *168*, 595;

10: M. D. Yoder, F. A. Jurnak; *Plant Physiol.* **1995**, *107*, 349;

11: O. Mayans, M. Scott, I. Connerton, T. Gravesen, J. Benen, J. Visser, R. Pickersgill, J. Jenkins; *Structure*, **1997**, *5*, 677;

12: J. Vitali, B. Schick, H. C. M. Kester, J. Visser, F. Jurnak; *Plant Physiol.* **1998**, *116*, 69;

13: R. Pickersgill, D. Smith, K. Worboys, J. Jenkins; *J. Biol. Chem.* **1998**, *273*, 24660;

14: R.D. Scavetta, S. R. Herron, A. T. Hotchkiss, N. Kita, N. T. Keen, J. A. E. Benen, H. C. M. Kester, J. Visser, F. Jurnak; *Plant Cell* **1999**, *11*, 1081;

15: M.Akita, A.Suzuki, T.Kobayashi,S.Ito, T.Yamane Crystallization And Preliminary X-Ray Analysis Of 2 High-Alkaline Pectate Lyase Acta Crystallogr., Sect.D V. 56 749 2000).

The crystal structures of a pectin methyl esterase (1QJV; Jenkins, J.; Mayans, O.; Smith, D.; Worboys, K.; Pickersgill, R.W. Journal of Molecular Biology, vol 305, 2001, 951-960) and a rhamnogalacturonase (1RMG; Petersen, T. N., Kauppinen, S., Larsen, S.: The crystal structure of rhamnogalacturonase A from Aspergillus aculeatus: a right-handed parallel beta helix. *Structure* 5 *pp.* 533 (1997)) have also been published.

Pectinases consist of an unusual backbone of parallel β-strands coiled in a large right-handed helix. The parallel β-helix contains three β-strands pr. turn (PB1, PB2, and PB3) and consecutive turns stack one on to another to form a super-helix. Two of the β-sheets form a β-sandwich folded against each other in an anti-parallel manner. The third parallel β-sheet is perpendicular to the β-sandwich, resulting in an L-

shaped cross-section. There is no direct sequence repetition in the β-helix, however a typical characteristic of the domain is that the side-chains of residues at corresponding positions in consecutive β-strands stack directly upon each other. The stacks can be of aliphatic (typically leucine, isoleucine and valine residues), hydrogen-bonded (typically asparagine residues, known as an asparagine ladder), or aromatic (typically tyrosine and phenylalanine residues) character. Stack amino acid side chains are found both within and outside the parallel β-helix, forming a linear arrangement parallel to the axis of the β helix.

The three β-sheets are separated by turns, termed T1 (between PB1 and PB2), T2 (between PB2 and PB3, introducing a 90° change of backbone orientation), and T3 (between PB3 and PB1). It is within these regions that the largest diversity among the different pectinases is found, the most conserved regions being the β-sheets PB2 and PB3 and the T2 turn. There is a large variety in the length of these turns, ranging from only two amino acids to tens of amino acids. The T3 turns are commonly lengthy and of more complex formation and constitute a loop region which together with the β-helix (primarily PB1) confines the substrate binding crevice.

The N-terminal end of the parallel β-helix domain is capped by an α-helix that is structurally conserved although the sequence conservation is undetectable. The C-terminal end of the β-helix is terminated by a loop structure with no specific conservation. The N-terminal tail packs against PB2 while the C-terminal tail lies across PB2 ending in a highly structurally (but not sequentially) conserved, amphipathic α-helix, with the hydrophobic part packing against the T2 turn.

In the bottom of the pronounced substrate-binding cleft calcium binds to three aspartate residues, two of which are conserved for all pectate lyases and one that can also be glutamate. In addition, two arginines, one lysine and a proline all facing the substrate-binding cleft are conserved in the pectinase family. Mutation of the aspartates (one can be

mutated to glutamate), the arginines or the lysine destroys the catalytic activity, however the exact catalytic mechanism is not fully understood.

A second cluster of invariant amino acids in the pectate lyases is located practically opposite to the Ca^{2+}-binding site, that is, on the other side of the β-helix domain packing against the N-terminus. Even though this iWiDH region is highly conserved throughout the pectinase family, the function of this is as yet unknown. It does not seem to be important for pectinolytic cleavage, but has been speculated to be involved in a second, yet unidentified, enzymatic function, or to be of importance in secretion of the enzyme always being of extra-cellular origin.

Hemicelluloses are the most complex group of non-starch polysaccharides in the plant cell wall. They consist of polymers of xylose, arabinose, galactose or mannose which are often highly branched and connected to other cell wall structures. Thus a multitude of enzymes is needed to degrade these structures (Ward and Young op.cit.). Xylanase, galactanase, arabinanase, lichenase and mannanase are some hemicellulose degrading enzymes.

Endo- and exo-xylanases and accessory enzymes such as glucuronidases, arabinofuranosidases, acetyl xylan esterase and ferulic acid or coumaric acid esterase have been summarized by Kormelink (1992, Ph.D.-thesis, University of Wageningen, The Netherlands). They are produced by a wide variety of micro-organisms and have varying temperature and pH optima.

Like other cell wall degrading enzymes (CWDE'S) galactanases occur in many micro-organisms (Dekker and Richards (1976), Adv. Carbohydrat. Chem. Biochem. 32, 278-319). In plant cell walls two types of arabinogalactans are present: type I 1,4 .beta.-galactans and type II 1,3/1,6 .beta.-galactans which have a branched backbone (Stephen (1983). In: The Polysaccharides. G. O. Aspinael (ed.). Ac. Press, New York, pp. 97-193). Both types of galactans require their own type of endo enzyme to be degraded. It can be expected that other enzymes, such as arabinan-degrading enzymes and exo-galactanases play a role in the degradation of arabinogalactans.

The hemicellulose 1,3-1,4-.beta.-glucan is a cell wall component present in cereal (barley, oat, wheat and rye) endosperm. The amount of .beta.-glucan in cereal endosperm varies between 0.7-8%. It is an unbranched polysaccharide built from cellotriose and cellotetraose residues linked by a 1,3-glucosidic bond. The ratio tri/tetra saccharose lies between 1.9 and 3.5.

Lichenase (EC 3.2.1.73) hydrolyse 1,4-beta-D-glucosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds. Lichenase reacts not on beta-D-glucans containing only 1,4-bonds such as for example in cellulose. Thus, damage of cellulose fibers in fabrics does not occur by the application of lichenase. Lichenases are produced by bacteria like B. amyloliguefaciens, B. circulans, B. licheniformis and plants (Bielecki S. et al. Crit. Rev. in Biotechn. 10(4), 1991, 275-304).

Arabinans consist of a main chain of .alpha.-L-arabinose subunits linked (.alpha.-(1->5) to another. Side chains are linked .alpha.-(1->3) or sometimes .alpha.-(1->2) to the main .alpha.-(1->5)-L-arabinan backbone. In apple, for example, one third of the total arabinose is present in the side chains. The molecular weight of arabinan is normally about 15 kDa.

Arabinan-degrading enzymes are known to be produced by a variety of plants and micro-organisms. Three enzymes obtainable from A.niger have been cloned by molecular biological techniques (EP-A-506190). Also arabinosidase from bacteria such as Bacteroides has been cloned (Whitehead and Hespell (1990). J. Bacteriol. 172, 2408).

Galactomannans are storage polysaccharides found in the seeds of Leguminosae. Galactomannans have a linear (1-->4)-.beta.-mannan backbone and are substituted with single (1-->6).alpha.-galactose residues. For example in guar gum the ratio mannose/galactose is about 2 to 1. Galactomannans are applied as thickeners in food products like dressings and soups.

Mannanase enzymes are described in PCT application WO 93/24622.

Glucomannan consists of a main chain of glucose and

mannose. The main chain may be substituted with galactose and acetyl groups; mannanases can be produced by a number of microorganisms, including bacteria and fungi.

To summarise, it can be said that a large number of plant cell wall degrading enzymes exist, produced by different organisms. Depending on their source the enzymes differ in substrate specificity, pH and temperature optima, V_{max}, K_m etc. The complexity of the enzymes reflects the complex nature of plant cell walls, which differ strongly between plant species and within species between plant tissues.

It is an object of the present invention to provide a cell-wall degrading enzyme variant, especially a pectin degrading enzyme variant, which exhibits improved performance over the known microbial cell-wall degrading enzymes when applied e.g. in detergents or in textile industry processes.

SUMMARY OF THE INVENTION

The inventors have now found that certain amino acid substitutions in cell-wall degrading enzymes having a structure including a β-helix result in enzyme variants having improved performance in the neutral or alkaline pH range, especially improved thermostability when determined by DSC (Disc Scanning Calorimetry) or by a Pad-Steam application test.

In a preferred embodiment of the invention, variants of the *Bacillus licheniformis* pectate lyase (EC 4.2.2.2) encoded by SEQ ID NO: 1 exhibit improved properties over the parent pectate lyase, the improved properties being advantageous when the enzyme is applied industrially. The inventors have provided such variants by having succeeded in identifying certain positions in the protein sequence in which positions the naturally occurring amino acid residue may be substituted or deleted or in which positions one or more amino acid residues may be inserted with the purpose of providing an improved pectate lyase variant, and have further provided a method of constructing cell-wall degrading enzyme variants with improved performance in industrial applications.

Accordingly, in a first aspect the present invention relates to a variant of a cell-wall degrading enzyme having a

beta-helix structure, which variant holds at least one substituent in a position determined by (i) identifying all residues potentially belonging to a stack; (ii) characterising the stack as interior or exterior; (iii) characterising the stack as polar (typically asparagine, serine, threonine) or hydrophobic (either aliphatic: leucine, isoleucine or valine; or aromatic/heteroaromatic: phenylalanine, tyrosine, histidine, and less often tryptophan) based on the dominating characteristics of the parent or wild-type enzyme stack residues and/or its orientation relative to the beta-helix (interior or exterior); (iv) optimising all stack positions of a stack either to hydrophobic aliphatic amino acids, hydrophobic aromatic/heteroaromatic amino acids (preferably histidine alone, tyrosine and phenylalanine alone or in combination) or polar amino acids (preferably asparagine) by allowing mutations within one or all positions to amino acids belonging to one of these groups; (v) measuring thermostability of the variants by DSC or an application-related assay such as a Pad-Steam application test; and (vi) selecting the stabilized variants. Alternatively, the variants may be provided by scanning the X-ray structure for positions that may be mutated into a proline residue; and mutating at least one of these positions into a proline; or by scanning the x-ray structure for positions that may be mutated into cysteine residues in order for these to form disulfide bridges and thereby stabilize the structure; and mutate at least one of these positions into a cysteine; or by initiating molecular dynamics calculations specifying different temperatures using the x-ray structure.

In a preferred embodiment, the invention relates to a variant of a wild-type parent pectate lyase (EC 4.2.2.2) having the conserved amino acid residues D111, D141 or E141, D145, K165, R194 and R199, optionally also W123, D125 and H126, when aligned with the pectate lyase comprising the amino acid sequence of SEQ ID NO: 2, in which the variant is substituted in at least one position selected from the group consisting of the positions 41, 55, 71, 72, 82, 83, 90, 100, 102, 114, 129, 133, 136, 144, 160, 163, 167, 168, 169, 189, 192, 197, 198,

200, 203, 207, 220, 222, 230, 232, 236, 237, 238, 244, 246, 261, 262, 265, 269, 282, 283, 284, 285, 288 and 289 . It is believed that the novel enzyme will be classified according to the Enzyme Nomenclature in the Enzyme Class EC 4.2.2.2. However, it should be noted that it is contemplated that the pectate lyase variant of the invention also exhibits catalytic activity on pectin (which may be esterified) besides the activity on pectate and polygalacturonides conventionally attributed to enzymes belonging to EC 4.2.2.2.

Within another aspect, the present invention provides an isolated polynucleotide molecule prepared from the DNA molecule comprising the DNA sequence of SEQ ID NO:1 by conventional methods such as site-directed mutagenesis.

Within yet another aspect of the invention there is provided an expression vector comprising the following operably linked elements: (a) a transcription promoter, (b) the polynucleotide molecule of the invention, (c) degenerate nucleotide sequences of (a) or (b); and a transcription terminator.

Within yet another aspect of the present invention there is provided a cultured cell into which has been introduced an expression vector as disclosed above, wherein said cell expresses the polypeptide encoded by the DNA segment.

Within another aspect of the present invention there is provided an enzyme composition comprising the pectate lyase variant of the invention in combination with other enzymes.

Within another aspect of the present invention there are provided methods for producing a polypeptide according to the invention comprising culturing a cell into which has been introduced an expression vector as disclosed above, whereby said cell expresses a polypeptide encoded by the DNA segment and recovering the polypeptide.

In comparison with the wild-type cell-wall degrading enzyme, especially a wild-type pectate lyase, it is contemplated that the variant of the invention exhibits increased thermal stability, either due to further stabilization of the β-helix structure of the protein by amino acid substitution in positions within the aliphatic and

aromatic stacks of amino acid side chains, or to further stabilization of the binding cleft or the C-terminal turn. Increased thermostability of an enzyme is indeed very useful in many industrial applications which advantageously can be carried out at a temperature above the temperature optimum for the enzymatic activity of the wild-type enzyme.

The cell-wall degrading enzyme variant of the invention is useful for the treatment of cellulosic material, especially cellulose-containing fiber, yarn, woven or non-woven fabric, treatment of mechanical paper-making pulps or recycled waste paper, and for retting of fibres. The treatment can be carried out during the processing of cellulosic material into a material ready for garment manufacture or fabric manufacture, e.g. in the desizing or scouring step; or during industrial or household laundering of such fabric or garment.

Accordingly, in further aspects the present invention relates to a detergent composition comprising an enzyme variant having substantial cell-wall degrading activity; and to use of the enzyme variant of the invention for the treatment of cellulose-containing fibers, yarn, woven or non-woven fabric.

The enzyme variant of the invention, especially the pectate lyase variant, is very effective for use in an enzymatic scouring process in the preparation of cellulosic material e.g. for proper response in subsequent dyeing operations.

THE DRAWING

Figure 1 is a multiple sequence alignment of pectate lyases derived from *Bacillus licheniformis* (pel_bacli), *Bacillus subtilis* (pel_bacsu) and *Erwinia chrysanthemi* (pel_erwch). The sequences were aligned using the align3d method of Modeller 5o (Ali, A.; T.L. Blundell, "Definition of general topological equivalence in protein structures: A procedure involving comparison of properties and relationships through simulated annealing and dynamic programming," *J. Mol. Biol.*, **212**, 403-428 (1990)) module of the Insight 2000 molecular modelling package (Biosym Inc.). Default parameters were employed using simple alignment of the sequences and the public PDB files as well as

the one enclosed here.

The figure was produced using the program ESPript (Gouet, P., Courcelle, E., Stuart, D. and Metoz, F. *Bioinformatics*, **15**, 305-308 (1999)), employing the Blosum matrix.

Appendix 1 shows the structural coordinates of the *Bacillus licheniformis* pectate lyase comprising the amino acid sequence of SEQ ID NO: 2.

DETAILED DESCRIPTION OF THE INVENTION

PROTEIN NUMBERING

In the context of this invention, a specific numbering of amino acid residue positions in cell-wall degrading enzymes, especially pectate lyase enzymes, is employed. For example, by aligning the amino acid sequences of known pectate lyases it is possible to unambiguously allot an amino acid position number to any amino acid residue in any pectate lyase enzyme, if its amino acid sequence is known.

In Figure 1, a number of selected amino acid sequences of pectate lyases of different microbial origin are aligned.

Using the numbering system originating from the amino acid sequence of the pectate lyase obtained from the strain *Bacillus licheniformis*, ATCC 14580, disclosed in SEQ ID NO: 2, aligned with the amino acid sequence of a number of other pectate lyases, it is possible to indicate the position of an amino acid residue in a pectate lyase enzyme unambiguously.

In describing the various cell-wall degrading enzyme variants produced or contemplated according to this invention, the following nomenclatures are adapted for ease of reference:

[Original amino acid; Position; Substituted amino acid]

Accordingly, the substitution of serine with isoleucine in position 72 is designated as S72I.

Multiple mutations are separation by addition marks ("+"), e.g. M169I + F198V, representing mutations in positions 169 and 198 substituting methionine (M) with isoleucine (I), and phenylalanine (F) with valine (V), respectively.

All positions referred to herein by pectate lyase numbering refer, unless otherwise stated, to the numbering described above, and are determined relative to the amino acid sequence of the pectate lyase derived from *Bacillus licheniformis*, ATCC 14580.

DEFINITIONS

Prior to discussing this invention in further detail, the following terms will first be defined.

The term "wild-type enzyme" denotes an enzyme, which is endogenous to a naturally occurring microorganism such as a fungus or a bacterium found in Nature.

The term "ortholog" (or "species homolog") denotes a polypeptide or protein obtained from one species that has homology to an analogous polypeptide or protein from a different species.

The term "paralog" denotes a polypeptide or protein obtained from a given species that has homology to a distinct polypeptide or protein from that same species.

The term "expression vector" denotes a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of interest operably linked to additional segments that provide for its transcription. Such additional segments may include promoter and terminator sequences, and may optionally include one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, and the like. Expression vectors are generally derived from plasmid or viral DNA, or may contain elements of both. The expression vector of the invention may be any expression vector that is conveniently subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which the vector it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector existing as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g. a plasmid. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into

which it has been integrated.

The term "recombinant expressed" or "recombinantly expressed" used herein in connection with expression of a polypeptide or protein is defined according to the standard definition in the art. Recombinant expression of a protein is generally performed by using an expression vector as described immediately above.

The term "isolated", when applied to a polynucleotide molecule, denotes that the polynucleotide has been removed from its natural genetic milieu and is thus free of other extraneous or unwanted coding sequences, and is in a form suitable for use within genetically engineered protein production systems. Such isolated molecules are those that are separated from their natural environment and include cDNA and genomic clones. Isolated DNA molecules of the present invention are free of other genes with which they are ordinarily associated, but may include naturally occurring 5' and 3' untranslated regions such as promoters and terminators. The identification of associated regions will be evident to one of ordinary skill in the art (see for example, Dynan and Tijan, Nature 316:774-78, 1985). The term "an isolated polynucleotide" may alternatively be termed "a cloned polynucleotide".

When applied to a protein/polypeptide, the term "isolated" indicates that the protein is found in a condition other than its native environment. In a preferred form, the isolated protein is substantially free of other proteins, particularly other homologous proteins (*i.e.* "homologous impurities" (see below)). It is preferred to provide the protein in a greater than 40% pure form, more preferably greater than 60% pure form. Even more preferably it is preferred to provide the protein in a highly purified form, i.e., greater than 80% pure, more preferably greater than 95% pure, and even more preferably greater than 99% pure, as determined by SDS-PAGE.

The term "isolated protein/polypeptide may alternatively be termed "purified protein/polypeptide".

The term "homologous impurities" means any impurity (e.g. another polypeptide than the polypeptide of the invention) which

originate from the homologous cell where the polypeptide of the invention is originally obtained from.

The term "obtained from" as used herein in connection with a specific microbial source, means that the polynucleotide and/or polypeptide produced by the specific source, or by a cell in which a gene from the source have been inserted.

The term "operably linked", when referring to DNA segments, denotes that the segments are arranged so that they function in concert for their intended purposes, e.g. transcription initiates in the promoter and proceeds through the coding segment to the terminator

The term "polynucleotide" denotes a single- or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. Polynucleotides include RNA and DNA, and may be isolated from natural sources, synthesized *in vitro*, or prepared from a combination of natural and synthetic molecules.

The term "complements of polynucleotide molecules" denotes polynucleotide molecules having a complementary base sequence and reverse orientation as compared to a reference sequence. For example, the sequence 5' ATGCACGGG 3' is complementary to 5' CCCGTGCAT 3'.

The term "degenerate nucleotide sequence" denotes a sequence of nucleotides that includes one or more degenerate codons (as compared to a reference polynucleotide molecule that encodes a polypeptide). Degenerate codons contain different triplets of nucleotides, but encode the same amino acid residue (i.e., GAU and GAC triplets each encode Asp).

The term "promoter" denotes a portion of a gene containing DNA sequences that provide for the binding of RNA polymerase and initiation of transcription. Promoter sequences are commonly, but not always, found in the 5' non-coding regions of genes.

The term "secretory signal sequence" denotes a DNA sequence that encodes a polypeptide (a "secretory peptide") that, as a component of a larger polypeptide, directs the larger polypeptide through a secretory pathway of a cell in which it is synthesized. The larger peptide is commonly cleaved to

remove the secretory peptide during transit through the secretory pathway.

The term "pectin" denotes pectate, polygalacturonic acid, and pectin which may be esterified to a higher or lower degree.

The term "pectinase" denotes a pectinase enzyme defined according to the art where pectinases are a group of enzymes that cleave glycosidic linkages of pectic substances mainly poly(1,4-alpha-D-galacturonide and its derivatives (see reference Sakai et al., Pectin, pectinase and protopectinase: production, properties and applications, pp 213-294 in: Advances in Applied Microbiology vol:39,1993).

Preferably a pectinase of the invention is a pectinase enzyme which catalyzes the random cleavage of alpha-1,4-glycosidic linkages in pectic acid also called polygalacturonic acid by transelimination such as the enzyme class polygalacturonate lyase (EC 4.2.2.2) (PGL) also known as poly(1,4-alpha-D-galacturonide) lyase also known as pectate lyase.

The term "thermostability" or "thermal stability" is intended to mean the stability of the protein to thermal influence. All enzyme proteins destabilizes and eventually degrades with increasing temperature, each enzyme protein having a certain temperature range wherein the protein is stable and retains its enzymatic activity. Increased thermostability means that the enzyme protein may retain its enzymatic activity and/or exhibit a higher relative activity at increased temperatures.

HOW TO USE A SEQUENCE OF THE INVENTION TO GET OTHER RELATED SEQUENCES

The disclosed sequence information herein relating to a polynucleotide sequence encoding a wild-type pectate lyase can be used as a tool to identify other homologous pectate lyases. For instance, polymerase chain reaction (PCR) can be used to amplify sequences encoding other homologous pectate lyases from a variety of microbial sources, in particular of different *Bacillus* species.

ASSAY FOR ACTIVITY TEST

A polypeptide variant of the invention having pectate lyase activity may be tested for pectate lyase activity according to standard test procedures known in the art, such as by applying a solution to be tested to 4 mm diameter holes punched out in agar plates containing 0.2% AZCL galactan (Megazyme, Australia).

ENZYME VARIANTS AND THE CONSTRUCTION THEREOF

In a preferred embodiment, the invention provides a variant of a parent cell-wall degrading enzymes having a β-helix structure, especially a pectate lyase (EC 4.2.2.2) variant, which retains the major enzymatic activity of the parent enzyme and has improved performance in industrial applications; and a method of constructing the variant. Thermostability and detergent compatibility are examples of enzyme properties, which may influence the performance of the enzyme in industrial applications such as commercial and domestic laundering of textiles and treatment of new textile fabric.

The method of constructing the variants of the invention comprises the steps of i) analyzing the structure of the parent enzyme in order to identify at least one amino acid residue or at least one structural part of the parent enzyme which is believed to influence the enzymatic properties of the parent enzyme as evaluated on the basis of structural or functional considerations, ii) constructing a variant which, compared to the parent enzyme, has been modified in the amino acid residue or structural part identified in i) so as to improve performance of the enzyme in textile applications, and, optionally, iii) testing the performance of the enzyme variant.

A model structure can be created using the "model" routine of Modeller 5o (ali, A.; T.L. Blundell, "Definition of general topological equivalence in protein structures: A procedure involving comparison of properties and relationships through simulated annealing and dynamic programming," *J. Mol. Biol.*, 212, 403-428 (1990)) module of the Insight 2000 molecular modelling package (Biosym Inc.). Required input is a sequence

alignment in pir format of the protein to be modelled to one or more homologues sequences where the crystal structure is available. The sequence alignment can be calculated by using ClustalW/ClustalX and standard parameters (ClustalX: Thompson,J.D., Gibson,T.J., Plewniak,F., Jeanmougin,F. and Higgins,D.G. (1997) The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Research, 24:4876-4882. ClustalW: Thompson, J.D., Higgins, D.G. and Gibson, T.J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. Nucleic Acids Research, 22:4673-4680.). Different refinement levels are determined by the MD_LEVEL keyword, and can typically be set to refine2 (default is less laborious and can also be employed). If further refinements are necessary this can be fulfilled by a minimisation of the structure using a molecular dynamics program such as CHARMm (Brooks et al, J. Computational Chemistry 4, 187 (1983)) possibly subjected to a (short) dynamics run followed by a second minimisation.

The inventors have found that cell-wall degrading enzyme variants, especially pectate lyases variants, having a stabilized beta-helix structure may exhibit improved performance in textile applications. In a preferred embodiment of the invention, the stabilized beta-helix structure may be obtained by determining the stack residues of the parent enzyme, followed by substitution of one or more stack residues. For example, the stack positions may be optimised by:

(i) Identifying all residues potentially belonging to a stack (the stack-residue positions for the *Bacillus licheniformis* pectate lyase comprising the amino acid sequence of SEQ ID NO: 2 are identified below);

(ii) Characterising the stack as interior or exterior;

(iii) Characterising the stack as polar (typically asparagine, glutamine, serine, threonine) or hydrophobic (either aliphatic: leucine, isoleucine or valine; or aromatic/heteroaromatic: phenylalanine, tyrosine, histidine, and less often tryptophan) based on the

dominating characteristics of the parent or wild-type enzyme stack residues and/or its orientation relative to the beta-helix (interior or exterior);

(iv) Optimising all stack positions of a stack either to hydrophobic aliphatic amino acids, hydrophobic aromatic amino acids (preferably histidine alone, tyrosine and phenylalanine alone or in combination) or polar amino acids (preferably asparagine) by allowing mutations within one or all positions to amino acids belonging to one of these groups;

(v) Measuring thermostability of the variants by DSC or an application-related assay such as a Pad-Steam application test; and

(vi) Selecting the stabilized variants.

A stack residue is defined as one of the following, based on the X-ray crystallography structure of the enzyme or a high-quality homology-build model:

(i) A residue of a β-strand (according to the output of the DSSP program, version July 1995 (Kabsch, W. and Sander, C., Biopolymers 22 (1983), 2577-2637), which β-strand is part of a sheet composed of more than two β-strands; or

(ii) A residue without secondary structure but which is linking two β-sheet regions horizontally; or

(iii) A residue of a T2 turn composed by no more than two amino acid residues; or

(iv) A residue having a C_α-atom in line with an already determined stack (i.e. visually it is clearly part of the stack); or

(v) A residue which, upon alignment of the amino acid sequence with SEQ ID NO: 2 or the structure as defined by the structural coordinates of Appendix 1, has a stack residue position as defined for the pectate lyase enzyme of SEQ ID NO:2.

Based on this procedure, the following residues are identified as stack-residues in the *Bacillus licheniformis* pectate lyase comprising the amino acid sequence of SEQ ID NO:2

and having the structural coordinates (X-ray structure) disclosed in Appendix 1:

Q22, T23, V24, T25, L45, K46, I47, Y48, T52, I53, T54, I63, D64, V65, K66, V68, S69, N70, V71, S72, I73, V74, E81, L82, K83, I87, K88, I89, W90, A92, N93, N94, I95, I96, I97, R98, N99, L100, K101, I102, H103, E104, I113, G114, I115, E116, S119, K120, N121, I122, W123, V124, D125, H126, N127, E128, I129, Y130, F144, D145, V146, K147, A150, E151, Y152, I153, T154, F155, S156, W157, N158, Y159, V160, H161, D162, G163, M167, L168, M169, T180, I181, T182, F183, H184, H185, N186, W187, F188, E189, N190, L191, P196, S197, F198, E202, G203, H204, I205, Y206, N207, N208, Y209, F210, N211, K212, I213, I218, N219, S220, R225, I226, R227, I228, E229, N230, N231, L232, F233, E234, N235, A236, I240, V241, Y250, W251, H252, V253, S254, N255, N256, K257, F258, V259, N260, S261

Preferred stack positions for substitution are:

155, 183, 23, 46, 72, 96, 123, 154, 182, 204, 227, 252, 22, 45, 203, 251, 152, 180, 202, 225, 250, 69, 93, 120, 151, 68, 92, 119, 150, 66, 90, 116, 147, 169, 198, 220, 64, 88, 114, 168, 197, 219, 241, 144, 167, 163, 191, 213, 236, 261, 104, 162, 190, 212, 235, 260, 54, 83, 103, 130, 161, 189, 211, 234, 259, 52, 81, 101, 128, 159, 187, 209, 232, 257, 100, 126, 157, 185, 25, 48, 74, 98, 125, 156, 184, 206, 229 and 254.

In another preferred embodiment of the invention, the stabilized beta-helix structure may be obtained by scanning the x-ray structure for positions that may be mutated into a proline residue; this can e.g. be done using the SUGPRO routine in the modelling program Whatif or by the method described in the international patent application published as WO92/19726.

Using the X-ray structure of Appendix 1, i.e. of the native *Bacillus licheniformis* pectate lyase, the following proline positions and proline substitution positions were identified by using the Whatif program:

40	(40)	ASN		22.03 -->	1.34 **
41	(41)	ALA	T	25.49 -->	0.63 **
44	(44)	PRO		11.11 -->	0.49 *
55	(55)	THR	T	22.74 -->	0.83 **
64	(64)	ASP	S	13.24 -->	0.21 *

```
118 ( 118) PRO  T   19.36 -->    -0.39 *
133 ( 133) LEU  T   11.74 -->    -0.11 *
136 ( 136) ASP      28.31 -->     2.25 ***
137 ( 137) LYS  T   28.09 -->     0.42 *
164 ( 164) TRP  S   21.92 -->     0.14 *
173 ( 173) ASP  T   12.66 -->    -0.46 *
196 ( 196) PRO  T    0.70 -->     1.43 **
239 ( 239) PRO       0.00 -->     0.54 **
248 ( 248) PRO      25.11 -->    -0.13 *
269 ( 269) SER      15.16 -->     0.72 **
275 ( 275) PRO       3.83 -->     0.77 **
283 ( 283) ASN      27.33 -->     3.82 *****
284 ( 284) VAL  T    3.11 -->     0.99 **
288 ( 288) LYS  H   22.93 -->     0.43 *
289 ( 289) SER  H   18.98 -->     1.11 **
```

Using the X-ray structure of Appendix 1, i.e. of the native *Bacillus licheniformis* pectate lyase, the following proline positions and proline substitution positions were identified by using the angle algorithm disclosed in WO92/19726 (at which position(s) the dihedral angles φ (phi) constitute values within the interval [-90°<φ<-40°], preferably the dihedral angles φ (phi) and ψ (psi) constitute values within the intervals [-90°<φ<-40°] and [-180°<ψ<-150° or -80<ψ<10 or 100<ψ<180], and which position(s) is/are not located in regions in which the enzyme is characterized by possessing α-helical or β-sheet structure):

```
 5 L  -65.6  129.0
 8 F  -50.9  -30.9 G
 9 A  -74.9  -10.7 G
10 A  -86.6   -9.4 G
19 E  -69.7  144.2 T
38 N  -76.3    8.5 T
39 K  -68.2  133.5
40 N  -81.8  117.6
41 A  -53.6  -21.7 T
44 P  -63.2  146.0
55 T  -70.5  -19.8 S
56 S  -73.8  -32.8 T
```

59	S	-81.7	7.2	S
61	S	-80.3	-8.8	S
109	D	-76.1	-6.3	T
112	A	-64.5	-52.6	S
117	G	-70.0	159.7	S
118	P	-81.5	128.5	S
136	D	-53.9	155.4	
137	K	-66.3	-23.9	T
139	Y	-63.0	-45.4	T
142	G	-71.7	160.4	
166	S	-71.6	-69.9	
171	S	-61.4	-31.2	S
173	D	-65.5	0.2	T
179	R	-65.6	140.0	
214	I	-62.9	-56.7	S
224	A	-65.3	144.7	
239	P	-63.3	-26.7	
246	S	-64.5	-30.6	S
248	P	-74.3	159.8	B
264	S	-69.0	115.0	
266	P	-54.6	134.3	
269	S	-88.7	146.3	
275	P	-58.3	138.8	
278	S	-88.4	159.0	
282	D	-78.1	153.4	
283	N	-60.1	133.4	
284	V	-55.6	-28.6	T
285	D	-72.8	-15.7	T
297	V	-85.1	157.8	T

Accordingly, preferred variants hold a proline residue in one or more of the following positions: 5, 8, 9, 10, 19, 38, 39, 40, 41, 44, 55, 56, 59, 61, 64, 109, 112, 117, 118, 133, 136, 137, 139, 142, 164, 166, 171, 173, 179, 196, 214, 224, 239, 246, 248, 264, 266, 269, 275, 278, 282, 283, 284, 285, 288, 289, 297.

In yet another preferred embodiment of the invention, the stabilized beta-helix structure may be obtained by scanning the x-ray structure for positions that may be mutated into cysteine

residues in order for these to form disulfide bridges and thereby stabilize the structure. This can be accomplished using the SUGCYS routine in the modelling program Whatif or by a method calculating Cβ-Cβ distances (glycines are mutated to alanines in order to have a Cβ-atom), preferably between 3.6 and 4.2 Å with a minimum sequence space of 2 amino acid residues.

In yet another preferred embodiment of the invention, the stabilized beta-helix structure may be obtained by initiating molecular dynamics calculations specifying different temperatures using the x-ray structure. By comparing the output thereof, regions potentially initiating thermal unfolding may be identified. Molecular dynamics runs may be performed e.g. using CHARMm (supplied by MSI) or NAMD (supplied by the Theoretical Biophysics Group at the University of Illinois) employing the X-ray structure including crystal waters and embedded in an equilibrated box of TIP3 water molecules, using periodic boundary conditions. The calculations may consist of a heating run of 30 ps followed by 1 ns simulation, using the following set-up parameters for all dynamics calculations: A time step of 1 fs (SHAKE algorithm applied to all hydrogen bonds) and a cut-off radius of 13Å with the gradient of the electrostatic potential reduced to zero by a force switching function applied from 8 to 12Å and the van der Waals potential shifted to zero. The stability of the simulations can be judged by monitoring the root-mean-square displacement (RMSD) of Cα-atoms as well as of all atoms, the radius of gyration (RGYR), and the solvent accessible surface.

As mentioned above, microbial pectate lyases may exhibit a low degree of sequence homology, but do share a number of highly conserved amino acid residues: D111, either D141 or E141, and D145 (Calcium-binding aspartates (glutamate)); R194 and R199 (binding-cleft arginines); K165 (lysine) and P196 (proline). Further, the sequence region in positions 122-126 is conserved by having the residues iWvDH, wherein i and v independently of each other are isoleucine, valine or leucine. These conserved positions may form the basis for aligning any wild-type microbial pectate lyase with the *Bacillus*

licheniformis pectate lyase comprising the amino acid sequence of SEQ ID NO:2 and having the structural coordinates (X-ray structure) disclosed in Appendix 1 and, in the wild-type pectate lyase), determine amino acid residues which may be optimized based on any of the methods described above. However, it should be noted that the conserved amino acid residues in positions 122-126 may be substituted without any loss of pectate lyase activity in the variant enzyme.

For example, it is contemplated that the above methods are useful for obtaining thermostabilized variants of other cell-wall degrading enzymes either having a known X-ray structure or a contemplated structure, which can be aligned with the structure in Appendix 1. Examples of crystallized cell-wall degrading enzymes with a published X-ray structure are *Bacillus* pectate lyases, especially *Bacillus subtilis* and *Bacillus licheniformis* pectate lyase, and *Erwinia chrysanthemi* pectate lyase. Figure 1 shows an alignment of the amino acid sequences of *Bacillus subtilis* pectate lyase (pel_bacsu), *Bacillus licheniformis* pectate lyase (pel_bacli), and of *Erwinia* pectate lyase (pel_erwch), which clearly identifies target positions for amino acid substitution according to the method of the present invention. Another example of a cell-wall degrading enzyme having a structure, which can be aligned with the structure in Appendix 1, is *Bacillus agaradhaerens* pectate lyase as disclosed in WO99/27084.

POLYNUCLEOTIDES

Within preferred embodiments of the invention it is contemplated that an isolated polynucleotide variant of the invention will hybridize to similar sized regions of the corresponding variant of SEQ ID NO:1, or a sequence complementary thereto, under at least medium stringency conditions, preferably high stringency conditions.

In particular polynucleotides of the invention will hybridize to a denatured double-stranded DNA probe comprising either the full variant sequence corresponding to positions 1-909 of SEQ ID NO:1 with proper sequence alterations corresponding to actual amino acid substitutions made or any

probe comprising a variant subsequence thereof having a length of at least about 100 base pairs under at least medium stringency conditions, but preferably at high stringency conditions as described in detail below. Suitable experimental conditions for determining hybridization at medium, or high stringency between a nucleotide probe and a homologous DNA or RNA sequence involves presoaking of the filter containing the DNA fragments or RNA to hybridize in 5 x SSC (Sodium chloride/Sodium citrate, Sambrook et al. 1989) for 10 min, and prehybridization of the filter in a solution of 5 x SSC, 5 x Denhardt's solution (Sambrook et al. 1989), 0.5 % SDS and 100 µg/ml of denatured sonicated salmon sperm DNA (Sambrook et al. 1989), followed by hybridization in the same solution containing a concentration of 10ng/ml of a random-primed (Feinberg, A. P. and Vogelstein, B. (1983) Anal. Biochem. 132:6-13), 32P-dCTP-labeled (specific activity higher than 1 x 109 cpm/µg) probe for 12 hours at ca. 45°C. The filter is then washed twice for 30 minutes in 2 x SSC, 0.5 % SDS at least 60°C (medium stringency), still more preferably at least 65°C (medium/high stringency), even more preferably at least 70°C (high stringency), and even more preferably at least 75°C (very high stringency).

Molecules to which the oligonucleotide probe hybridizes under these conditions are detected using an X-ray film.

As previously noted, the isolated polynucleotides of the present invention include DNA and RNA. Methods for isolating DNA and RNA are well known in the art. DNA and RNA encoding genes of interes can be cloned in Gene Banks or DNA libraries by means of methods known in the art.

Polynucleotides encoding polypeptides having pectate lyase activity of the invention are then identified and isolated by, for example, hybridization or PCR.

Species homologues of the wild-type pectate lyase used in preparation of the pectate lyase variants of the invention can be cloned using information and compositions provided by the present invention in combination with conventional cloning techniques. For example, DNA can be cloned using chromosomal DNA obtained from a cell type that expresses the protein.

Suitable sources of DNA can be identified by probing Northern blots with probes designed from the sequences disclosed herein. A library is then prepared from chromosomal DNA of a positive cell line. A DNA encoding a polypeptide having pectate lyase activity of the invention can then be isolated by a variety of methods, such as by probing with a complete or partial DNA or with one or more sets of degenerate probes based on the disclosed sequences. A DNA can also be cloned using the polymerase chain reaction, or PCR (Mullis, U.S. Patent 4,683,202), using primers designed from the sequences disclosed herein. Within an additional method, the DNA library can be used to transform or transfect host cells, and expression of the DNA of interest can be detected with an antibody (monoclonal or polyclonal) raised against the pectate lyase cloned from *B.licheniformis*, ATCC 14580, expressed and purified as described in Materials and Methods, or by an activity test relating to a polypeptide having pectate lyase activity. Similar techniques can also be applied to the isolation of genomic clones.

The polypeptide encoding part of the DNA sequence cloned into plasmid pSJ1678 present in *Escherichia coli* DSM 11789 and/or an analogue DNA sequence of the invention may be cloned from a strain of the bacterial species *Bacillus licheniformis*, preferably the strain ATCC 14580, producing the enzyme with pectin degrading activity, or another or related organism as described herein.

Alternatively, the analogous sequence may be constructed on the basis of the DNA sequence obtainable from the plasmid present in *Escherichia coli* DSM 11789, *e.g* be a sub-sequence thereof, and/or by introduction of nucleotide substitutions which do not give rise to another amino acid sequence of the pectat lyase encoded by the DNA sequence, but which corresponds to the codon usage of the host organism intended for production of the enzyme, or by introduction of nucleotide substitutions which may give rise to a different amino acid sequence (*i.e.* a variant of the pectin degrading enzyme of the invention).

POLYPEPTIDES

The sequence of amino acids no. 1-302 of SEQ ID No 2 is a mature pectate lyase sequence corresponding to a wild-type pectate lyase from the species *Bacillus licheniformis*.

The sequence of amino acids no. 1-302 of SEQ ID No 7 is a mature pectate lyase sequence corresponding to the variant M169I + F198V of the pectate lyase from the species *Bacillus licheniformis*.

The sequence of amino acids no. 1-302 of SEQ ID No 8 is a mature pectate lyase sequence corresponding to the variant M169I + F198V + S72I of the pectate lyase from the species *Bacillus licheniformis*.

The present invention also provides pectate lyase variants of polypeptides that are substantially homologous to the polypeptides of SEQ ID NO:7 or SEQ ID NO:8 and their species homologs (paralogs or orthologs) with the proviso that the amino acid residues of the following positions of SEQ ID NO:7 or SEQ ID NO:8 are conserved: 111, 141, 145, 165, 169, 194, 196, 198 and 199. Optionally, the amino acid residues of positions 123, 125 and 126 are also conserved, but amino acid substitutions in any of these positions may be made without loss of catalytic, i.e. pectate lyase, activity. The term "substantially homologous" is used herein to denote polypeptides having 70%, more preferably at least 85%, and even more preferably at least 90%, sequence identity to the sequence shown in SEQ ID NO:7 or SEQ ID NO:8 or their orthologs or paralogs. Such polypeptides will more preferably be at least 95% identical, and most preferably 98% or more identical to the sequence shown in SEQ ID NO:7 or SEQ ID NO:8 or its orthologs or paralogs. Percent sequence identity is determined by conventional methods, by means of computer programs known in the art such as GAP provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711) as disclosed in Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453, which is hereby incorporated by reference in its entirety. GAP is used with the following settings for polypeptide

sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1.

Sequence identity of polynucleotide molecules is determined by similar methods using GAP with the following settings for DNA sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3.

The wild-type pectate lyase is preferably derived from a microorganism, preferably from a bacterium, an archea or a fungus, especially from a bacterium such as a bacterium belonging to *Bacillus*, preferably to an alkalophilic *Bacillus* strain which may be selected from the group consisting of the species *Bacillus licheniformis* and highly related *Bacillus* species in which all species preferably are at least 95%, even more preferably at least 98%, homologous to *Bacillus licheniformis* based on aligned 16S rDNA sequences.

Substantially homologous wild-type proteins and polypeptides are characterized as having one or more amino acid substitutions, deletions or additions. These changes are preferably of a minor nature, that is conservative amino acid substitutions (see Table 2) and other substitutions that do not significantly affect the folding or activity of the protein or polypeptide; small deletions, typically of one to about 30 amino acids; and small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue, a small linker peptide of up to about 20-25 residues, or a small extension that facilitates purification (an affinity tag), such as a poly-histidine tract, protein A (Nilsson et al., EMBO J. 4:1075, 1985; Nilsson et al., Methods Enzymol. 198:3, 1991. See, in general Ford et al., Protein Expression and Purification 2: 95-107, 1991, which is incorporated herein by reference. DNAs encoding affinity tags are available from commercial suppliers (e.g., Pharmacia Biotech, Piscataway, NJ; New England Biolabs, Beverly, MA).

However, even though the changes described above preferably are of a minor nature, such changes may also be of a larger nature such as fusion of larger polypeptides of up to 300 amino acids or more both as amino- or carboxyl-terminal extensions.

Table 1

Conservative amino acid substitutions

Basic:	arginine
	lysine
Acidic:	glutamic acid
	aspartic acid
Polar:	glutamine
	asparagine
	serine
	threonine
Hydrophobic:	leucine
	isoleucine
	valine
Aromatic/	
Heteroaromatic:	phenylalanine
	tryptophan
	tyrosine
	histidine
Small:	glycine
	alanine
	methionine

In addition to the 20 standard amino acids, non-standard amino acids (such as 4-hydroxyproline, 6-*N*-methyl lysine, 2-aminoisobutyric acid, isovaline and a-methyl serine) may be substituted for amino acid residues of a wild-type polypeptide. A limited number of non-conservative amino acids, amino acids that are not encoded by the genetic code, and unnatural amino acids may be substituted for amino acid residues. "Unnatural amino acids" have been modified after protein synthesis, and/or have a chemical structure in their side chain(s) different from that of the standard amino acids. Unnatural amino acids can be chemically synthesized, or preferably, are commercially available, and include pipecolic acid, thiazolidine carboxylic acid, dehydroproline, 3- and 4-methylproline, and 3,3-dimethylproline.

Essential amino acids in the pectate lyase polypeptides of the present invention can be identified according to procedures

known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, Science 244: 1081-1085, 1989). In the latter technique, single alanine mutations are introduced at every residue in the molecule, and the resultant mutant molecules are tested for biological activity (*i.e* pectate lyase activity) to identify amino acid residues that are critical to the activity of the molecule. See also, Hilton et al., J. Biol. Chem. 271:4699-4708, 1996. The active site of the enzyme or other biological interaction can also be determined by physical analysis of structure, as determined by such techniques as nuclear magnetic resonance, crystallography, electron diffraction or photoaffinity labeling, in conjunction with mutation of putative contact site amino acids. See, for example, de Vos et al., Science 255:306-312, 1992; Smith et al., J. Mol. Biol. 224:899-904, 1992; Wlodaver et al., FEBS Lett. 309:59-64, 1992. The identities of essential amino acids can also be inferred from analysis of homologies with polypeptides which are related to a polypeptide according to the invention.

Multiple amino acid substitutions can be made and tested using known methods of mutagenesis, recombination and/or shuffling followed by a relevant screening procedure, such as those disclosed by Reidhaar-Olson and Sauer (Science 241:53-57, 1988), Bowie and Sauer (Proc. Natl. Acad. Sci. USA 86:2152-2156, 1989), WO95/17413, or WO 95/22625. Briefly, these authors disclose methods for simultaneously randomizing two or more positions in a polypeptide, or recombination/shuffling of different mutations (WO95/17413, WO95/22625), followed by selecting for functional a polypeptide, and then sequencing the mutagenized polypeptides to determine the spectrum of allowable substitutions at each position. Other methods that can be used include phage display (e.g., Lowman et al., Biochem. 30:10832-10837, 1991; Ladner et al., U.S. Patent No. 5,223,409; Huse, WIPO Publication WO 92/06204) and region-directed mutagenesis (Derbyshire et al., Gene 46:145, 1986; Ner et al., DNA 7:127, 1988).

Mutagenesis/shuffling methods as disclosed above can be combined with high-throughput, automated screening methods to

detect activity of cloned, mutagenized polypeptides in host cells. Mutagenized DNA molecules that encode active polypeptides can be recovered from the host cells and rapidly sequenced using modern equipment. These methods allow the rapid determination of the importance of individual amino acid residues in a polypeptide of interest, and can be applied to polypeptides of unknown structure.

Using the methods discussed above, one of ordinary skill in the art can identify and/or prepare a variety of polypeptides that are substantially homologous to residues 1 to 302 of SEQ ID NO: 2 and retain the pectate lyase activity of the wild-type protein.

However, the very same methods are also useful for providing the pectate lyase variants of the invention having more advantageous properties than the wild-type protein. Using these methods, the present inventors have identified a number of positions in which the wild-type pectate lyase of SEQ ID NO:2 may advantageously by substituted in order to prepare variants with improved properties.

Preferred pectate lyase variants of the inventions are substituted in one or more of the following positions (numbering relative to SEQ ID NO:2): 41, 55, 71, 72, 82, 83, 90, 100, 102, 114, 129, 133, 136, 144, 160, 163, 167, 168, 169, 189, 192, 197, 198, 200, 203, 207, 220, 222, 230, 232, 236, 237, 238, 244, 246, 261, 262, 265, 269, 282, 283, 284, 285, 288 and 289.

Further examples of preferred variants are those holding a proline residue in one or more of the following positions (numbering relative to SEQ ID NO:2): 5, 8, 9, 10, 19, 38, 39, 40, 41, 44, 55, 56, 59, 61, 64, 109, 112, 117, 118, 133, 136, 137, 139, 142, 164, 166, 171, 173, 179, 196, 214, 224, 239, 246, 248, 264, 266, 269, 275, 278, 282, 283, 284, 285, 288, 289, 297.

In a preferred embodiment of the present invention, the *Bacillus licheniformis* pectate lyase variant comprises at least one substituted amino acid residue selected from the group consisting of A41P, T55P, V71N, S72I,T, L82I, K83N,H, W90H, L100N, I102F, G114N, L129F, L133N, D136A,P,S,T,V, F144V, V160F,

G163L,H,I, M167F,I,S, L168N, M169I, E189H,N, N192Y, S197N, F198V, F200N,Y, G203V,A, N207S, S220,V, M222N,Y, N230E, L232N, A236V, K237N, D238N, Y244D, S246R,P, S261I, R262E, M265K, S269P, D282H, N283P, D284P, D285G, K288P and S289P. It is at present contemplated that one or more of these substitutions either alone or in combination increase the thermostability of the pectate lyase variant when compared to the wild-type enzyme.

Preferred multiple substitutions in the aliphatic and aromatic stacks of amino acid side chains believed to stabilize the β-helix structure are:

M169I + F198V
M169I + F198V + S220I
M169I + F198V + S220V
S197N + L168N
S197N + L168N + G114N
F200N + M222N
F200Y + M222Y,

and other preferred substitutions in the stacks are K83N, M167F,I, E189H,N, G163L, L100N, S72I and V71N.

Preferred multiple substitutions believed to stabilize the C-terminal turn are:

N283P + D285G
D282H + N283P + D284P
D282H + N283P + D284P + K288P

Preferred multiple substitutions believed to stabilize the binding cleft are:

K237N + D238N
K237N + D238N + R262E
Y244D + S246R
N207S + N230E,

and other preferred substitutions are D136Y, N192Y and R262E.

The pectate lyase variant of the invention may, in addition to the enzyme core comprising the catalytically domain, also comprise a cellulose binding domain (CBD), the cellulose binding domain and enzyme core (the catalytically active domain) of the enzyme being operably linked. The cellulose binding domain (CBD) may exist as an integral part

of the encoded enzyme, or a CBD from another origin may be introduced into the pectin degrading enzyme thus creating an enzyme hybrid. In this context, the term "cellulose-binding domain" is intended to be understood as defined by Peter Tomme et al. "Cellulose-Binding Domains: Classification and Properties" in "Enzymatic Degradation of Insoluble Carbohydrates", John N. Saddler and Michael H. Penner (Eds.), ACS Symposium Series, No. 618, 1996. This definition classifies more than 120 cellulose-binding domains into 10 families (I-X), and demonstrates that CBDs are found in various enzymes such as cellulases, xylanases, mannanases, arabinofuranosidases, acetyl esterases and chitinases. CBDs have also been found in algae, e.g. the red alga *Porphyra purpurea* as a non-hydrolytic polysaccharide-binding protein, see Tomme et al., *op.cit.* However, most of the CBDs are from cellulases and xylanases, CBDs are found at the N and C termini of proteins or are internal. Enzyme hybrids are known in the art, see e.g. WO 90/00609 and WO 95/16782, and may be prepared by transforming into a host cell a DNA construct comprising at least a fragment of DNA encoding the cellulose-binding domain ligated, with or without a linker, to a DNA sequence encoding the pectin degrading enzyme and growing the host cell to express the fused gene. Enzyme hybrids may be described by the following formula:

CBD - MR - X

wherein CBD is the N-terminal or the C-terminal region of an amino acid sequence corresponding to at least the cellulose-binding domain; MR is the middle region (the linker), and may be a bond, or a short linking group preferably of from about 2 to about 100 carbon atoms, more preferably of from 2 to 40 carbon atoms; or is preferably from about 2 to to about 100 amino acids, more preferably of from 2 to 40 amino acids; and X is an N-terminal or C-terminal region of the pectin degrading enzyme of the invention.

PROTEIN PRODUCTION

The polypeptides of the present invention, including full-length proteins, fragments thereof and fusion proteins, can be

produced in genetically engineered host cells according to conventional techniques. Suitable host cells are those cell types that can be transformed or transfected with exogenous DNA and grown in culture, and include bacteria, fungal cells, and cultured higher eukaryotic cells. Bacterial cells, particularly cultured cells of gram-positive organisms, are preferred. Gram-positive cells from the genus of Bacillus are especially preferred, such as *Bacillus subtilis, Bacillus lentus, Bacillus brevis, Bacillus stearothermophilus, Bacillus alkalophilus, Bacillus amyloliquefaciens, Bacillus coagulans, Bacillus circulans, Bacillus lautus, Bacillus thuringiensis, Bacillus agaradherens,* or in particular *Bacillus licheniformis.*

Techniques for manipulating cloned DNA molecules and introducing exogenous DNA into a variety of host cells are disclosed by Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley and Sons, Inc., NY, 1987; and (Bacillus subtilis and Other Gram-Positive Bacteria, Sonensheim et al., 1993, American Society for Microbiology, Washington D.C.), which are incorporated herein by reference.

In general, a DNA sequence encoding a pectate lyase of the present invention is operably linked to other genetic elements required for its expression, generally including a transcription promoter and terminator within an expression vector. The vector will also commonly contain one or more selectable markers and one or more origins of replication, although those skilled in the art will recognize that within certain systems selectable markers may be provided on separate vectors, and replication of the exogenous DNA may be provided by integration into the host cell genome. Selection of promoters, terminators, selectable markers, vectors and other elements is a matter of routine design within the level of ordinary skill in the art. Many such elements are described in the literature and are available through commercial suppliers.

To direct a polypeptide into the secretory pathway of a host cell, a secretory signal sequence (also known as a leader sequence, prepro sequence or pre sequence) is provided in the

expression vector. The secretory signal sequence may be that of the polypeptide, or may be derived from another secreted protein or synthesized *de novo*. Numerous suitable secretory signal sequences are known in the art and reference is made to (Bacillus subtilis and Other Gram-Positive Bacteria, Sonenshein et al., 1993, American Society for Microbiology, Washington D.C.; and Cutting, S. M.(eds.) "Molecular Biological Methods for Bacillus". John Wiley and Sons, 1990) for further description of suitable secretory signal sequences especially for secretion in a Bacillus host cell. The secretory signal sequence is joined to the DNA sequence in the correct reading frame. Secretory signal sequences are commonly positioned 5' to the DNA sequence encoding the polypeptide of interest, although certain signal sequences may be positioned elsewhere in the DNA sequence of interest (see, e.g., Welch et al., U.S. Patent No. 5,037,743; Holland et al., U.S. Patent No. 5,143,830).

Transformed or transfected host cells are cultured according to conventional procedures in a culture medium containing nutrients and other components required for the growth of the chosen host cells. A variety of suitable media, including defined media and complex media, are known in the art and generally include a carbon source, a nitrogen source, essential amino acids, vitamins and minerals. Media may also contain such components as growth factors or serum, as required. The growth medium will generally select for cells containing the exogenously added DNA by, for example, drug selection or deficiency in an essential nutrient which is complemented by the selectable marker carried on the expression vector or co-transfected into the host cell.

The fermentation may be carried out by cultivation of the host cell under aerobic conditions in a nutrient medium containing carbon and nitrogen sources together with other essential nutrients, the medium being composed in accordance with the principles of the known art. The medium may be a complex rich medium or a minimal medium. The nitrogen source may be of inorganic and/or organic nature. Suitable inorganic nitrogen sources are nitrates and ammonium salts. Among the organic nitrogen sources quite a number are used regularly in

fermentations. Examples are soybean meal, casein, corn, corn steep liquor, yeast extract, urea and albumin. Suitable carbon sources are carbohydrates or carbohydrate containing materials. Preferable the nutrient medium contains pectate, polygalacturonic acid and/or pectin esterified to a higher or lower degree as carbon source and/or inducer of pectinase production. Alternatively, the medium contains a pectin rich material such as soybean meal, apple pulp or citrus peel.

The cultivation may preferably be conducted at alkaline pH values such as at least pH 8 or at least pH 9, which can be obtained by addition of suitable buffers such as sodium carbonate or mixtures of sodium carbonate and sodium bicarbonate after sterilisation of the growth medium.

PROTEIN ISOLATION

When the expressed recombinant polypeptide is secreted the polypeptide may be purified from the growth media. Preferably the expression host cells are removed from the media before purification of the polypeptide (e.g. by centrifugation).

When the expressed recombinant polypeptide is not secreted from the host cell, the host cell are preferably disrupted and the polypeptide released into an aqueous "extract" which is the first stage of such purification techniques. Preferably the expression host cells are removed from the media before the cell disruption (e.g. by centrifugation).

The cell disruption may be performed by conventional techniques such as by lysozyme digestion or by forcing the cells through high pressure. See (Robert K. Scobes, Protein Purification, Second edition, Springer-Verlag) for further description of such cell disruption techniques.

Whether or not the expressed recombinant polypeptides (or chimeric polypeptides) is secreted or not it can be purified using fractionation and/or conventional purification methods and media.

Ammonium sulfate precipitation and acid or chaotrope extraction may be used for fractionation of samples. Exemplary purification steps may include hydroxyapatite, size exclusion, FPLC and reverse-phase high performance liquid chromatography.

Suitable anion exchange media include derivatized dextrans, agarose, cellulose, polyacrylamide, specialty silicas, and the like. PEI, DEAE, QAE and Q derivatives are preferred, with DEAE Fast-Flow Sepharose (Pharmacia, Piscataway, NJ) being particularly preferred. Exemplary chromatographic media include those media derivatized with phenyl, butyl, or octyl groups, such as Phenyl-Sepharose FF (Pharmacia), Toyopearl butyl 650 (Toso Haas, Montgomeryville, PA), Octyl-Sepharose (Pharmacia) and the like; or polyacrylic resins, such as Amberchrom CG 71 (Toso Haas) and the like. Suitable solid supports include glass beads, silica-based resins, cellulosic resins, agarose beads, cross-linked agarose beads, polystyrene beads, cross-linked polyacrylamide resins and the like that are insoluble under the conditions in which they are to be used. These supports may be modified with reactive groups that allow attachment of proteins by amino groups, carboxyl groups, sulfhydryl groups, hydroxyl groups and/or carbohydrate moieties. Examples of coupling chemistries include cyanogen bromide activation, N-hydroxysuccinimide activation, epoxide activation, sulfhydryl activation, hydrazide activation, and carboxyl and amino derivatives for carbodiimide coupling chemistries. These and other solid media are well known and widely used in the art, and are available from commercial suppliers.

Selection of a particular method is a matter of routine design and is determined in part by the properties of the chosen support. See, for example, Affinity Chromatography: Principles & Methods, Pharmacia LKB Biotechnology, Uppsala, Sweden, 1988.

Polypeptides of the invention or fragments thereof may also be prepared through chemical synthesis. Polypeptides of the invention may be monomers or multimers; glycosylated or non-glycosylated; pegylated or non-pegylated; and may or may not include an initial methionine amino acid residue.

Accordingly, in a further aspect, the present invention also relates to a method of producing the enzyme preparation of the invention, the method comprising culturing a microorganism capable of producing the pectate lyase variant under conditions permitting the production of the enzyme, and

recovering the enzyme from the culture. Culturing may be carried out using conventional fermentation techniques, e.g. culturing in shake flasks or fermentors with agitation to ensure sufficient aeration on a growth medium inducing production of the pectate lyase variant. The growth medium may contain a conventional N-source such as peptone, yeast extract or casamino acids, a reduced amount of a conventional C-source such as dextrose or sucrose, and an inducer such as pectate or pectin or composit plant substrates such as cereal brans (e.g. wheat bran or rice husk). The recovery may be carried out using conventional techniques, e.g. separation of bio-mass and supernatant by centrifugation or filtration, recovery of the supernatant or disruption of cells if the enzyme of interest is intracellular, perhaps followed by further purification as described in EP 0 406 314 or by crystallization as described in WO 97/15660.

In yet another aspect, the present invention relates to an isolated pectate lyase variant having the properties described above and which is free from homologous impurities, and is produced using conventional recombinant techniques.

TRANSGENIC PLANTS

The present invention also relates to a transgenic plant, plant part or plant cell which has been transformed with a DNA sequence encoding the pectin degrading enzyme of the invention so as to express and produce this enzyme in recoverable quantities. The enzyme may be recovered from the plant or plant part. Alternatively, the plant or plant part containing the recombinant enzyme may be used as such.

The transgenic plant can be dicotyledonous or monocotyledonous, for short a dicot or a monocot. Examples of monocot plants are grasses, such as meadow grass (blue grass, Poa), forage grass such as festuca, lolium, temperate grass, such as Agrostis, and cereals, e.g. wheat, oats, rye, barley, rice, sorghum and maize (corn).

Examples of dicot plants are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous (family Brassicaceae), such as cauliflower, oil

seed rape and the closely related model organism Arabidopsis thaliana.

Examples of plant parts are stem, callus, leaves, root, fruits, seeds, and tubers. In the present context, also specific plant tissues, such as chloroplast, apoplast, mitochondria, vacuole, peroxisomes and cytoplasm are considered to be a plant part. Furthermore, any plant cell, whatever the tissue origin, is considered to be a plant part.

Also included within the scope of the invention are the progeny of such plants, plant parts and plant cells.

The transgenic plant or plant cell expressing the enzyme of the invention may be constructed in accordance with methods known in the art. In short the plant or plant cell is constructed by incorporating one or more expression constructs encoding the enzyme of the invention into the plant host genome and propagating the resulting modified plant or plant cell into a transgenic plant or plant cell.

Conveniently, the expression construct is a DNA construct which comprises a gene encoding the enzyme of the invention in operable association with appropriate regulatory sequences required for expression of the gene in the plant or plant part of choice. Furthermore, the expression construct may comprise a selectable marker useful for identifying host cells into which the expression construct has been integrated and DNA sequences necessary for introduction of the construct into the plant in question (the latter depends on the DNA introduction method to be used).

The choice of regulatory sequences, such as promoter and terminator sequences and optionally signal or transit sequences is determined, eg on the basis of when, where and how the enzyme is desired to be expressed. For instance, the expression of the gene encoding the enzyme of the invention may be constitutive or inducible, or may be developmental, stage or tissue specific, and the gene product may be targeted to a specific tissue or plant part such as seeds or leaves. Regulatory sequences are eg described by Tague et al, Plant, Phys., 86, 506, 1988.

For constitutive expression the 35S-CaMV promoter may be

used (Franck et al., 1980. Cell 21: 285-294). Organ-specific promoters may eg be a promoter from storage sink tissues such as seeds, potato tubers, and fruits (Edwards & Coruzzi, 1990. Annu. Rev. Genet. 24: 275-303), or from metabolic sink tissues such as meristems (Ito et al., 1994. Plant Mol. Biol. 24: 863-878), a seed specific promoter such as the glutelin, prolamin, globulin or albumin promoter from rice (Wu et al., Plant and Cell Physiology Vol. 39, No. 8 pp. 885-889 (1998)), a *Vicia faba* promoter from the legumin B4 and the unknown seed protein gene from *Vicia faba* described by Conrad U. et al, Journal of Plant Physiology Vol. 152, No. 6 pp. 708-711 (1998), a promotter from a seed oil body protein (Chen et al., Plant and cell physiology vol. 39, No. 9 pp. 935-941 (1998), the storage protein napA promoter from Brassica napus, or any other seed specific promoter known in the art, eg as described in WO 91/14772. Furthermore, the promoter may be a leaf specific promoter such as the rbcs promoter from rice or tomato (Kyozuka et al., Plant Physiology Vol. 102, No. 3 pp. 991-1000 (1993), the chlorella virus adenine methyltransferase gene promoter (Mitra, A. and Higgins, DW, Plant Molecular Biology Vol. 26, No. 1 pp. 85-93 (1994), or the aldP gene promoter from rice (Kagaya et al., Molecular and General Genetics Vol. 248, No. 6 pp. 668-674 (1995), or a wound inducible promoter such as the potato pin2 promoter (Xu et al, Plant Molecular Biology Vol. 22, No. 4 pp. 573-588 (1993).

A promoter enhancer element may be used to achieve higher expression of the enzyme in the plant. For instance, the promoter enhancer element may be an intron which is placed between the promoter and the nucleotide sequence encoding the enzyme. For instance, Xu et al. *op cit* disclose the use of the first intron of the rice actin 1 gene to enhance expression.

The selectable marker gene and any other parts of the expression construct may be chosen from those available in the art.

The DNA construct is incorporated into the plant genome according to conventional techniques known in the art, including *Agrobacterium*-mediated transformation, virus-mediated transformation, micro injection, particle bombardment,

biolistic transformation, and electroporation (Gasser et al, Science, 244, 1293; Potrykus, Bio/Techn. 8, 535, 1990; Shimamoto et al, Nature, 338, 274, 1989).

Presently, *Agrobacterium tumefaciens* mediated gene transfer is the method of choice for generating transgenic dicots (for review Hooykas & Schilperoort, 1992. Plant Mol. Biol. 19: 15-38), however it can also be used for transforming monocots, although other transformation methods are generally preferred for these plants. Presently, the method of choice for generating transgenic monocots is particle bombardment (microscopic gold or tungsten particles coated with the transforming DNA) of embryonic calli or developing embryos (Christou, 1992. Plant J. 2: 275-281; Shimamoto, 1994. Curr. Opin. Biotechnol. 5: 158-162; Vasil et al., 1992. Bio/Technology 10: 667-674). An alternative method for transformation of monocots is based on protoplast transformation as described by Omirulleh S, et al., Plant Molecular biology Vol. 21, No. 3 pp. 415-428 (1993).

Following transformation, the transformants having incorporated the expression construct are selected and regenerated into whole plants according to methods well known in the art.

ENZYME PREPARATION

In the present context, the term "enzyme preparation" is intended to mean either be a conventional enzymatic fermentation product, possibly isolated and purified, from a single species of a microorganism, such preparation usually comprising a number of different enzymatic activities; or a mixture of monocomponent enzymes, preferably enzymes derived from bacterial or fungal species by using conventional recombinant techniques, which enzymes have been fermented and possibly isolated and purified separately and which may originate from different species, preferably fungal or bacterial species; or the fermentation product of a microorganism which acts as a host cell for expression of a recombinant pectate lyase or pectate lyase variant, but which microorganism simultaneously produces other enzymes, e.g.

pectin lyases, proteases, or cellulases, being naturally occurring fermentation products of the microorganism, i.e. the enzyme complex conventionally produced by the corresponding naturally occurring microorganism.

The pectate lyase variant preparation of the invention may further comprise one or more enzymes selected from the group consisting of proteases, cellulases (endo-β-1,4-glucanases), β-glucanases (endo-β-1,3(4)-glucanases), lipases, cutinases, peroxidases, laccases, amylases, glucoamylases, pectinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xyloglucanases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, pectin methylesterases, cellobiohydrolases, transglutaminases; or mixtures thereof. In a preferred embodiment, one or more or all enzymes in the preparation is produced by using recombinant techniques, i.e. the enzyme(s) is/are mono-component enzyme(s) which is/are mixed with the other enzyme(s) to form an enzyme preparation with the desired enzyme blend.

IMMUNOLOGICAL CROSS-REACTIVITY

Polyclonal antibodies to be used in determining immunological cross-reactivity may be prepared by use of a purified pectate lyase enzyme. More specifically, antiserum against the pectate lyase of the invention may be raised by immunizing rabbits (or other rodents) according to the procedure described by N. Axelsen et al. in: A Manual of Quantitative Immunoelectrophoresis, Blackwell Scientific Publications, 1973, Chapter 23, or A. Johnstone and R. Thorpe, Immunochemistry in Practice, Blackwell Scientific Publications, 1982 (more specifically p. 27-31). Purified immunoglobulins may be obtained from the antisera, for example by salt precipitation ($(NH_4)_2SO_4$), followed by dialysis and ion exchange chromatography, *e.g.* on DEAE-Sephadex. Immunochemical characterization of proteins may be done either by Outcherlony double-diffusion analysis (O. Ouchterlony in: Handbook of Experimental Immunology (D.M. Weir, Ed.), Blackwell Scientific Publications, 1967, pp. 655-706), by

crossed immunoelectrophoresis (N. Axelsen et al., supra, Chapters 3 and 4), or by rocket immunoelectrophoresis (N. Axelsen et al., Chapter 2).

Use in the detergent industry

In further aspects, the present invention relates to a detergent composition comprising the pectate lyase variant or pectate lyase variant preparation of the invention, and to a process for machine treatment of fabrics comprising treating fabric during a washing cycle of a machine washing process with a washing solution containing the pectate lyase variant or pectate lyase variant preparation of the invention.

Typically, the detergent composition of the invention comprises conventional ingredients such as surfactants (anionic, nonionic, zwitterionic, amphoteric), builders, and other ingredients, e.g. as described in WO 97/01629 which is hereby incorporated by reference in its entirety.

Use in the textile and cellulosic fiber processing industries

The pectate lyase variant of the present invention can be used in combination with other carbohydrate degrading enzymes (for instance arabinanase, xyloglucanase, pectinase) for biopreparation of fibers or for cleaning of fibers in combination with detergents. Cotton fibers consist of a primary cell wall layer containing pectin and a secondary layer containing mainly cellulose. Under cotton preparation or cotton refining part of the primary cell wall will be removed. The present invention relates to either help during cotton refining by removal of the primary cell wall. Or during cleaning of the cotton to remove residual pectic substances and prevent graying of the textile.

In the present context, the term "cellulosic material" is intended to mean fibers, sewn and unsewn fabrics, including knits, wovens, denims, yarns, and toweling, made from cotton, cotton blends or natural or manmade cellulosics (e.g. originating from xylan-containing cellulose fibers such as from wood pulp) or blends thereof. Examples of blends are blends of cotton or rayon/viscose with one or more companion material

such as wool, synthetic fibers (e.g. polyamide fibers, acrylic fibers, polyester fibers, polyvinyl alcohol fibers, polyvinyl chloride fibers, polyvinylidene chloride fibers, polyurethane fibers, polyurea fibers, aramid fibers), and cellulose-containing fibers (e.g. rayon/viscose, ramie, hemp, flax/linen, jute, cellulose acetate fibers, lyocell).

The preparation of the present invention is useful in the cellulosic fiber processing industry for the pre-treatment or retting of fibers from hemp, flax or linen.

The processing of cellulosic material for the textile industry, as for example cotton fiber, into a material ready for garment manufacture involves several steps: spinning of the fiber into a yarn; construction of woven or knit fabric from the yarn and subsequent preparation, dyeing and finishing operations. Woven goods are constructed by weaving a filling yarn between a series of warp yarns; the yarns could be two different types. Knitted goods are constructed by forming a network of interlocking loops from one continuous length of yarn. The cellulosic fibers can also be used for non-woven fabric.

The preparation process prepares the textile for the proper response in dyeing operations. The sub-steps involved in preparation are

a. Desizing (for woven goods) using polymeric size like e.g. starch, CMC or PVA is added before weaving in order to increase the warp speed; This material must be removed before further processing.

b. Scouring, the aim of which is to remove non-cellulosic material from the cotton fiber, especially the cuticle (mainly consisting of waxes) and primary cell wall (mainly consisting of pectin, protein and xyloglucan). A proper wax removal is necessary for obtaining a high wettability, being a measure for obtaining a good dyeing. Removal of the primary cell wall - especially the pectins - improves wax removal and ensures a more even dyeing. Further this improves the whiteness in the bleaching process. The main chemical used in scouring is sodium hydroxide in high concentrations, up to 70 g/kg cotton and at high temperatures, 80-95°C; and

c. Bleaching; normally the scouring is followed by a bleach using hydrogen peroxide as the oxidizing agent in order to obtain either a fully bleached (white) fabric or to ensure a clean shade of the dye.

A one step combined scour/bleach process is also used by the industry. Although preparation processes are most commonly employed in the fabric state; scouring, bleaching and dyeing operations can also be done at the fiber or yarn stage.

The processing regime can be either batch or continuous with the fabric being contacted by the liquid processing stream in open width or rope form. Continuous operations generally use a saturator whereby an approximate equal weight of chemical bath per weight of fabric is applied to the fabric, followed by a heated dwell chamber where the chemical reaction takes place. A washing section then prepares the fabric for the next processing step. Batch processing generally takes place in one processing bath whereby the fabric is contacted with approximately 8 -15 times its weight in chemical bath. After a reaction period, the chemicals are drained, fabric rinsed and the next chemical is applied. Discontinuous pad-batch processing involves a saturator whereby an approximate equal weight of chemical bath per weight of fabric is applied to the fabric, followed by a dwell period, which, in the case of cold pad-batch, might be one or more days.

Woven goods are the prevalent form of textile fabric construction. The weaving process demands a "sizing" of the warp yarn to protect it from abrasion. Starch, polyvinyl alcohol (PVA), carboxymethyl cellulose, waxes and acrylic binders are examples of typical sizing chemicals used because of availability and cost. The size must be removed after the weaving process as the first step in preparing the woven goods. The sized fabric in either rope or open width form is brought in contact with the processing liquid containing the desizing agents. The desizing agent employed depends upon the type of size to be removed. For PVA sizes, hot water or oxidative processes are often used. The most common sizing agent for cotton fabric is based upon starch. Therefore most often, woven cotton fabrics are desized by a combination of hot water, the

enzyme α-amylase to hydrolyze the starch and a wetting agent or surfactant. The cellulosic material is allowed to stand with the desizing chemicals for a "holding period" sufficiently long to accomplish the desizing. The holding period is dependent upon the type of processing regime and the temperature and can vary from 15 minutes to 2 hours, or in some cases, several days. Typically, the desizing chemicals are applied in a saturator bath which generally ranges from about 15°C to about 55°C. The fabric is then held in equipment such as a "J-box" which provides sufficient heat, usually between about 55°C and about 100°C, to enhance the activity of the desizing agents. The chemicals, including the removed sizing agents, are washed away from the fabric after the termination of the holding period.

In order to ensure a high whiteness or a good wettability and resulting dyeability, the size chemicals and other applied chemicals must be thoroughly removed. It is generally believed that an efficient desizing is of crucial importance to the following preparation processes: scouring and bleaching.

The scouring process removes much of the non-cellulosic compounds naturally found in cotton. In addition to the natural non-cellulosic impurities, scouring can remove dirt, soils and residual manufacturing introduced materials such as spinning, coning or slashing lubricants. The scouring process employs sodium hydroxide or related causticizing agents such as sodium carbonate, potassium hydroxide or mixtures thereof. Generally an alkali stable surfactant is added to the process to enhance solubilization of hydrophobic compounds and/or prevent their redeposition back on the fabric. The treatment is generally at a high temperature, 80°C - 100°C, employing strongly alkaline solutions, pH 13-14, of the scouring agent. Due to the non-specific nature of chemical processes not only are the impurities but the cellulose itself is attacked, leading to damages in strength or other desirable fabric properties. The softness of the cellulosic fabric is a function of residual natural cotton waxes. The non-specific nature of the high temperature strongly alkaline scouring process cannot

discriminate between the desirable natural cotton lubricants and the manufacturing introduced lubricants. Furthermore, the conventional scouring process can cause environmental problems due to the highly alkaline effluent from these processes. The scouring stage prepares the fabric for the optimal response in bleaching. An inadequately scoured fabric will need a higher level of bleach chemical in the subsequent bleaching stages.

The bleaching step decolorizes the natural cotton pigments and removes any residual natural woody cotton trash components not completely removed during ginning, carding or scouring. The main process in use today is an alkaline hydrogen peroxide bleach. In many cases, especially when a very high whiteness is not needed, bleaching can be combined with scouring.

In the examples below it is shown that the scouring step can be carried out using the pectate lyase or pectate lyase preparation of the present invention a temperature of about 50°C - 80°C and a pH of about 7-11, thus substituting or supplementing the highly causticizing agents. An optimized enzymatic process ensures a high pectin removal and full wettability.

Degradation or modification of plant material

The enzyme or enzyme preparation according to the invention is preferably used as an agent for degradation or modification of plant cell walls or any pectin-containing material originating from plant cells walls due to the high plant cell wall degrading activity of the pectate lyase variant of the invention.

The pectate lyase variant of the present invention may be used alone or together with other enzymes like glucanases, pectinases and/or hemicellulases to improve the extraction of oil from oil-rich plant material, like soy-bean oil from soy-beans, olive-oil from olives or rapeseed-oil from rape-seed or sunflower oil from sunflower.

The pectate lyase variant of the present invention may be used for separation of components of plant cell materials. Of particular interest is the separation of sugar or starch rich plant material into components of considerable commercial

interest (like sucrose from sugar beet or starch from potato) and components of low interest (like pulp or hull fractions). Also, of particular interest is the separation of protein-rich or oil-rich crops into valuable protein and oil and invaluable hull fractions, The separation process may be performed by use of methods known in the art.

The pectate lyase variant of the invention may also be used in the preparation of fruit or vegetable juice in order to increase yield, and in the enzymatic hydrolysis of various plant cell wall-derived materials or waste materials, e.g. from wine or juice production, or agricultural residues such as vegetable hulls, bean hulls, sugar beet pulp, olive pulp, potato pulp, and the like.

The plant material may be degraded in order to improve different kinds of processing, facilitate purification or extraction of other component than the galactans like purification of pectins from citrus, improve the feed value, decrease the water binding capacity, improve the degradability in waste water plants, improve the conversion of plant material to ensilage, etc.

By means of an enzyme preparation of the invention it is possible to regulate the consistency and appearance of processed fruit or vegetables. The consistency and appearance has been shown to be a product of the actual combination of enzymes used for processing, i.e. the specificity of the enzymes with which the pectate lyase variant of the invention is combined. Examples include the production of clear juice e.g. from apples, pears or berries; cloud stable juice e.g. from apples, pears, berries, citrus or tomatoes; and purees e.g. from carrots and tomatoes.

The pectate lyase variant of the invention may be used in modifying the viscosity of plant cell wall derived material. For instance, the pectate lyase variant may be used to reduce the viscosity of feed containing galactan and to promote processing of viscous galactan containing material. The viscosity reduction may be obtained by treating the galactan containing plant material with an enzyme preparation of the invention under suitable conditions for full or partial degradation of the galactan containing material

The pectate lyase variant can be used e.g. in combination with other enzymes for the removal of pectic substances from plant fibres. This removal is essential e.g. in the production of textile fibres or other cellulosic materials. For this purpose plant fibre material is treated with a suitable amount of the pectate lyase of the invention under suitable conditions for obtaining full or partial degradation of pectic substances associated with the plant fibre material.

Animal feed additive

Pectate lyase variants of the present invention may be used for modification of animal feed and may exert their effect either in vitro (by modifying components of the feed) or in vivo. The pectate lyase variant is particularly suited for addition to animal feed compositions containing high amounts of arabinogalactans or galactans, e.g. feed containing plant material from soy bean, rape seed, lupin etc. When added to the feed the pectate lyase variant significantly improves the in vivo break-down of plant cell wall material, whereby a better utilization of the plant nutrients by the animal is achieved. Thereby, the growth rate and/or feed conversion ratio (i.e. the weight of ingested feed relative to weight gain) of the animal is improved. For example the indigestible galactan is degraded by pectate lyase, e.g. in combination with ß-galactosidase, to galactose or galactooligomers which are digestible by the animal and thus contribute to the available energy of the feed. Also, by the degradation of galactan the pectate lyase may improve the digestibility and uptake of non-carbohydrate feed constituents such as protein, fat and minerals.

For further description reference is made to PCT/DK 96/00443 and a working example herein.

Wine and juice processing

The enzyme or enzyme preparation of the invention may be used for de-pectinization and viscosity reduction in vegetable or fruit juice, especially in apple or pear juice. This may be accomplished by treating the fruit or vegetable juice with an enzyme preparation of the invention in an amount effective for

degrading pectin-containing material contained in the fruit or vegetable juice.

The enzyme or enzyme preparation may be used in the treatment of mash from fruits and vegetables in order to improve the extractability or degradability of the mash. For instance, the enzyme preparation may be used in the treatment of mash from apples and pears for juice production, and in the mash treatment of grapes for wine production.

DETERMINATION OF CATALYTIC ACTIVITY OF PECTATE LYASE

The viscosity assay APSU

APSU units: The APSU assay measures the change in viscosity of a solution of polygalacturonic acid in the absence of added calcium ions.

A 5% w/v solution of sodium polygalacturonate (Sigma P-1879) is solubilised in 0.1 M glycine buffer, pH 10. 4 ml of this solution are preincubated for 5 min at 40 ?C. Then, 250 µl of the enzyme (or enzyme dilution) are added, after which the reaction is mixed for 10 sec on a mixer at the highest speed and incubated for 20 min at 40?C or at another temperature.

Viscosity is measured using a MIVI 600 viscometer (Sofraser, 45700 Villemandeur, France). Viscosity is measured as mV after 10 sec. For calculation of APSU units the following standard curve is used:

APSU/ml	mV
0.00	300
4.00	276
9.00	249
14.00	227
19.00	206
24.00	188
34.00	177
49.00	163
99.00	168

MATERIALS AND METHODS

Strains

Bacillus licheniformis ATCC 14580.

B.subtilis PL2306. This strain is the B.subtilis DN1885 with disrupted apr and npr genes (Diderichsen, B., Wedsted, U., Hedegaard, L., Jensen, B. R., Sjøholm, C. (1990) Cloning of aldB, which encodes alpha-acetolactate decarboxylase, an exoenzyme from Bacillus brevis. J. Bacteriol., 172, 4315-4321) disrupted in the transcriptional unit of the known *Bacillus subtilis* cellulase gene, resulting in cellulase negative cells. The disruption was performed essentially as described in (Eds. A.L. Sonenshein, J.A. Hoch and Richard Losick (1993) *Bacillus subtilis* and other Gram-Positive Bacteria, American Society for microbiology, p.618).

Competent cells were prepared and transformed as described by Yasbin, R.E., Wilson, G.A. and Young, F.E. (1975) Transformation and transfection in lysogenic strains of *Bacillus subtilis*: evidence for selective induction of prophage in competent cells. J. Bacteriol, 121:296-304.

Plasmids

pMOL944:

This plasmid is a pUB110 derivative essentially containing elements making the plasmid propagatable in Bacillus subtilis, kanamycin resistance gene and having a strong promoter and signal peptide cloned from the amyL gene of *B.licheniformis* ATCC14580. The signal peptide contains a SacII site making it convenient to clone the DNA encoding the mature part of a protein in-fusion with the signal peptide. This results in the expression of a Pre-protein which is directed towards the exterior of the cell.

The plasmid was constructed by means of conventional genetic engineering techniques which are briefly described in the following.

Construction of pMOL944:

The pUB110 plasmid (McKenzie, T. et al., 1986, Plasmid 15:93-103) was digested with the unique restriction enzyme

NciI. A PCR fragment amplified from the amyL promoter encoded on the plasmid pDN1981 (P.L. Jørgensen et al., 1990, Gene, 96, p37-41.) was digested with NciI and inserted in the NciI digested pUB110 to give the plasmid pSJ2624.

The two PCR primers used have the following sequences:

LWN5494 5´-GTCGCCGGGGCGGCCGCTATCAATTGGTAACTGTATCTCAGC -3´

LWN5495 5´-GTCGCCCGGGAGCTCTGATCAGGTACCAAGCTTGTCGACCTGCAGAA TGAGGCAGCAAGAAGAT -3´

The primer #LWN5494 inserts a NotI site in the plasmid.

The plasmid pSJ2624 was then digested with SacI and NotI and a new PCR fragment amplified on amyL promoter encoded on the pDN1981 was digested with SacI and NotI and this DNA fragment was inserted in the SacI-NotI digested pSJ2624 to give the plasmid pSJ2670.

This cloning replaces the first amyL promoter cloning with the same promoter but in the opposite direction. The two primers used for PCR amplification have the following sequences:

#LWN5938 5`-GTCGGCGGCCGCTGATCACGTACCAAGCTTGTCGACCTGCAGAATG AGGCAGCAAGAAGAT -3´

#LWN5939 5`-GTCGGAGCTCTATCAATTGGTAACTGTATCTCAGC -3´

The plasmid pSJ2670 was digested with the restriction enzymes PstI and BclI and a PCR fragment amplified from a cloned DNA sequence encoding the alkaline amylase SP722 (disclosed in the International Patent Application published as WO95/26397 which is hereby incorporated by reference in its entirety) was digested with PstI and BclI and inserted to give the plasmid pMOL944. The two primers used for PCR amplification have the following sequence:

#LWN7864 5` -AACAGCTGATCACGACTGATCTTTTAGCTTGGCAC-3´

#LWN7901 5` -AACTGCAGCCGCGGCACATCATAATGGGACAAATGGG -3´

The primer #LWN7901 inserts a SacII site in the plasmid.

Genomic DNA preparation

Strain *Bacillus licheniformis* ATCC 14580 was propagated in liquid medium 3 as specified by ATCC (American Type Culture Collection, USA). After 18 hours incubation at 37°C and 300 rpm, the cells were harvested, and genomic DNA isolated by the method described by Pitcher et al. (Pitcher, D. G., Saunders, N. A., Owen, R. J. (1989). Rapid extraction of bacterial genomic DNA with guanidium thiocyanate. Lett. Appl. Microbiol., 8, 151-156).

The pectate lyase encoding DNA sequence of the invention was PCR amplified using the PCR primer set consisting of these two oligo nucleotides:

Pecl.B.lich.upper.SacII
5'-CTA ACT GCA GCC GCG GCA GCT TCT GCC TTA AAC TCG GGC -3'

Pecl.B.lich.lower.NotI
5'-GCG TTG AGA CGC GCG GCC GCT GAA TGC CCC GGA CGT TTC ACC -3'

Restriction sites SacII and NotII are underlined.

Chromosomal DNA isolated from *B.licheniformis* ATCC 14580 as described above was used as template in a PCR reaction using Amplitaq DNA Polymerase (Perkin Elmer) according to manufacturers instructions. The PCR reaction was set up in PCR buffer (10 mM Tris-HCl, pH 8.3, 50 mM KCl, 1.5 mM $MgCl_2$, 0.01 % (w/v) gelatin) containing 200 µM of each dNTP, 2.5 units of AmpliTaq polymerase (Perkin-Elmer, Cetus, USA) and 100 pmol of each primer

The PCR reactions was performed using a DNA thermal cycler (Landgraf, Germany). One incubation at 94°C for 1 min followed by thirty cycles of PCR performed using a cycle profile of denaturation at 94°C for 30 sec, annealing at 60°C for 1 min, and extension at 72°C for 2 min. Five-µl aliquots of the amplification product was analysed by electrophoresis in 0.7 % agarose gels (NuSieve, FMC). The appearance of a DNA fragment size 1.0 kb indicated proper amplification of the gene segment.

Subcloning of PCR fragment

Fortyfive-µl aliquots of the PCR products generated as described above were purified using QIAquick PCR purification kit (Qiagen, USA) according to the manufacturer's instructions. The purified DNA was eluted in 50 µl of 10mM Tris-HCl, pH 8.5. 5 µg of pMOL944 and twentyfive-µl of the purified PCR fragment was digested with SacII and NotI, electrophoresed in 0.8 % low gelling temperature agarose (SeaPlaque GTG, FMC) gels, the relevant fragments were excised from the gels, and purified using QIAquick Gel extraction Kit (Qiagen, USA) according to the manufacturer's instructions. The isolated PCR DNA fragment was then ligated to the SacII-NotI digested and purified pMOL944. The ligation was performed overnight at 16°C using 0.5 µg of each DNA fragment, 1 U of T4 DNA ligase and T4 ligase buffer (Boehringer Mannheim, Germany).

The ligation mixture was used to transform competent *B.subtilis* PL2306. The transformed cells were plated onto LBPG-10 µg/ml of Kanamycin plates. After 18 hours incubation at 37°C several clones were restreaked on fresh agar plates and also grown in liquid TY cultures with 10 µg/ ml kanamycin and incubated overnight at 37°C. Next day 1 ml of cells were used to isolate plasmid from the cells using the Qiaprep Spin Plasmid Miniprep Kit #27106 according to the manufacturers recommendations for *B.subtilis* plasmid preparations. This plasmid DNA was used as template for DNA sequencing.

One clone containing the pectate lyase gene was kept, this clone was termed MB541, and the pectate lyase expressing plasmid was denoted pMB541.

The DNA corresponding to the mature part of the pectate lyase was characterised by DNA sequencing by primerwalking, using the Taq deoxy-terminal cycle sequencing kit (Perkin-Elmer, USA), fluorescent labelled terminators and appropriate oligonucleotides as primers.

Analysis of the sequence data was performed according to Devereux *et al.* (1984) Nucleic Acids Res. 12, 387-395. The cloned DNA sequence was expressed in *B.subtilis* and the protein that appeared in the supernatant corresponded to the mature

protein represented in SEQ ID NO:2.

Media

TY (as described in Ausubel, F. M. et al. (eds.) "Current protocols in Molecular Biology". John Wiley and Sons, 1995).

LB agar (as described in Ausubel, F. M. et al. (eds.) "Current protocols in Molecular Biology". John Wiley and Sons, 1995).

LBPG is LB agar supplemented with 0.5% Glucose and 0.05 M potassium phosphate, pH 7.0

BPX media is described in EP 0 506 780 (WO 91/09129).

The following examples illustrate the invention.

EXAMPLE 1

Construction of Pectate Lyase variant (M169I, F198V)

The wild-type *B. licheniformis* pectate lyase encoded by SEQ ID NO: 1 is expressed in *B. subtilis* from a plasmid denoted pMB541, see Materials and Methods. This plasmid contains a fusion of the signal sequence from *B. licheniformis* alpha-amylase and the gene encoding the mature protein of *B. licheniformis* pectate lyase (SEQ ID NO: 2, wild-type pectate lyase), the expression of which is directed by the *B. licheniformis alpha-amylase promoter*. Further, the plasmid contains the origin of replication, *ori*, from plasmid pUB110 and the *cat* gene from plasmid pC194 conferring resistance towards chloramphenicol. A specific mutagenesis vector with a 1.2 kb pUC fragment inserted in the unique *Pst*I restriction site located between the nucleotide sequence coding for the signal sequence and the mature, was prepared. The important features of this vector, denoted pCA134 include an origin of replication derived from the pUC plasmids, the *cat* gene conferring resistance towards chloramphenicol and gene coding the mature part of the wild-type *B. licheniformis* pectate lyase.

After verification of the DNA sequence in variant plasmids, the *Pst*I-*Pst*I fragment from pUC is removed and the remaining part of the vector is ligated and transformed into the protease- and amylase-depleted *Bacillus subtilis* strain SHA273 (described in WO92/11357 and WO95/10603) in order to express the variant

enzyme.

In an attempt to improve the stability of said pectate lyase site-directed mutagenesis was carried out using the Mega-primer method as described by Sarkar and Sommer, 1990, BioTechniques 8: 404-407).

The *B. licheniformis* pectate lyase variant M169I+F198V was constructed by the use of the gene specific primer Pely01 (SEQ ID NO:4) and mutagenic primers Pely22 (SEQ ID NO:5) and Pely23 (SEQ ID NO:6) to amplify by PCR an approximately 470 bp DNA fragment from the pCA134 plasmid. The 470 bp fragment is purified from an agarose gel and used as a Mega-primer together with primer 113711 in a second PCR carried out on the same template.

The resulting approximately 1050 bp fragment is digested with restriction enzymes *Bcl*I and *Not*I and the resulting approximately 570 bp DNA fragment is purified and ligated with the pCA134 plasmid digested with the same enzymes. Competent *Bacillus subtilis* SHA273 (amylase and protease low) cells are transformed with the ligation, and Chloro-amphenicol resistant transformants are checked by DNA sequencing to verify the presence of the correct mutations on the plasmid.

Primer 113711:
5' GAAACAGCTATGACCATGATTACGCC 3' (SEQ ID NO: 3)
Primer Pely01:
5' CGACTGGCAATGCCGGGGCGG 3' (SEQ ID NO: 4)
Primer Pely22:
5' GGAAATCAATGCTGATCGGTTCATCGGACAGC 3' (SEQ ID NO: 5)
Primer Pely23:
5' CGTGTGCCGTCAGTACGTTTCGGAGGAGGC 3' (SEQ ID NO: 6)

EXAMPLE 2

Fermentation, purification and characterization of *Bacillus licheniformis* pectate lyase variant M169I, F198V

The clone obtained as described in Example 1 was grown in 25 x 200 ml BPX media with 10 µl/ml of Kanamycin in 500ml two baffled shake flasks for 5 days at 37°C at 300 rpm.

140 ml of shake flask culture fluid were diluted to 1000 ml with ion free water and applied to S-Sepharose (50 ml column equilibrated with 25 mM sodium acetate buffer pH 5.5). The pure pectate lyase variant was eluted using a NaCl gradient.

The pectate lyase variant gave a single band in SDS-PAGE of 35 kDa, exhibited 23 APSU units per mg protein, and a molar extinction coefficient of 57750.

The buffer of the pure enzyme was changed by size chromatography on a high load Superdex S200 column equilibrated with 0.1M EPPS buffer pH 8.0. DSC (Differential Scanning Calorimetry) was performed using a temperature increase of 1°C per minute. The pure pectate lyase variant unfolds at 77°C on a Microcalc calorimeter. In contrast hereto, the wild-type or parent pectate lyase enzyme melts at 69°C under identical conditions (pH 8). DSC was also performed using Glycin buffer, 0.68 mM $CaCl_2$ pH 10, and the pure pectate lyase variant unfolds at 68°C on a Microcalc calorimeter. In contrast hereto, the wild-type or parent pectate lyase enzyme melts at 60°C under identical conditions (pH 10).

EXAMPLE 3

Construction, fermentation, purification and characterization of further *Bacillus licheniformis* pectate lyase variants

By using the methods described in Example 1 and 2, the *Bacillus licheniformis* pectate lyase variants (relative to SEQ ID NO:2) of Table I below were prepared and subjected to DSC (Differential Scanning Calorimetry) at pH 10 or pH 8 using a temperature increase of 1°C per minute. The wild-type *Bacillus licheniformis* pectate lyase (SEQ ID NO:2) has a DSC unfolding temperature of 60°C (pH 10) and 70°C (pH 8).

Table I

Variant no.	Substitutions relative to SEQ ID NO:2	DSC unfolding temperature (°C)	
		pH 10	pH 8
1	M169I + F198V + E189H	67	
2	M169I + F198V + S72I	72	
3	M169I + F198V + F144V + M167I	70.1	
4	M169I + F198V + S72I + M265K	75.9	
5	M169I + F198V + S72I + G203V	74.7	
6	M169I + F198V + S72I + K83H	75.7	
7	M169I + F198V + S72T	66	
8	M169I + F198V + M167I	65.6	
9	M169I + F198V + S72I + L82I + I102F + L129F + V160F		76.8
10	M169I + F198V + T55P	70.8	
11	M169I + F198V + S269P	68.5	
12	D282H + N283P + D284P	66	
13	D282H + N283P + D284P + K288P	66	
14	M169I + F198V + N283P + D284P + K288P + S289P	69.7	
15	M169I + F198V + A41P	65	
16	M169I + F198V + D136P	66.8	
17	M169I + F198V + N283P	66.1	
18	M169I + F198V + D136S	75.8	78.6
19	M169I + F198V + D136T	68.6	
20	M169I + F198V + S72I + M265K	75.9	
21	M169I + F198V + S72I + K83N	75.7	

Variant 1-6 and 21: stacking positive; variant 7-9: stacking neutral; variant 10-14: proline positive; variant 15-17: proline neutral; variant 18-20: other positive.

By using the methods described in Example 1 and 2, the *Bacillus licheniformis* pectate lyase variants (relative to SEQ ID NO:2) of Table II below were also prepared.

Table II

Variant no.	Substitutions relative to SEQ ID NO:2
22	N207S
23	N230E
24	N207S + N230E
25	M169I + F198V + V71N
26	M169I + F198V + W90H
27	M169I + F198V + L100N
28	M169I + F198V + S72I + W90H
29	M169I + F198V + S72I + G163I
30	M169I + F198V + S72I + G203A
31	M169I + F198V + S72I + F144V + 167S
32	M169I + F198V + S72I + G163I + 236V + S261I
33	N283P + D285G

Variant no. 22-32: stacking, unknown; variant no. 33: proline, unknown

EXAMPLE 4

Pectate Lyase Treatment of Cellulosic Material: Effect of Pectate Lyase Variants vs. Wild-Type Pectate Lyase (SEQ ID NO: 2) on Residual Pectin

The activity of the pectate lyase variants M169I + F198V, M169I + F198V+S220V, M169I + F198V+D136A, M169I + F198V+T55P, all prepared according to Example 1, in textile preparation is determined by measuring the amount of pectin removed from the fabric after treating with the enzyme in a surfactant-buffer solution.

A. Materials

Fabric: Swatches (25.4 cm x 91.4 cm) of 100% carded cotton fabric from Test Fabrics, quality 428U (242 g/m^2) was used.

Equipment: A Labomat (Mathis, Switzerland) was used at a liquor ratio of 12.5:1 (12 g fabric in 150 ml buffer/enzyme solution).

Pectate lyase: Each of the pectate lyase variants M169I + F198V, M169I + F198V+S220V, M169I + F198V+D136A, M169I + F198V+T55P were used, formulated in a solution containing 10 mM

borate buffer and 0.2 % (w/w) non-ionic surfactant (Tergitol 15-S-12 from Union Carbide) and 0.1% (w/w) Geropon SS-O-75, pH 8.2. Samples were compared based on equal protein concentrations.

B. Procedures and Results

The test fabrics were impregnated with the aqueous solution containing the pectate lyase by a determined wet pick-up between 95-100%, and incubated for 15 minutes at 90°C followed by a continuously washing using the following rinse cycle:

Tank 1 - Tap water rinse at 90°C (overflow rinsing)

Tank 2 - Tap water rinse at 90°C (overflow rinsing)

Tank 3 - Tap water rinse at 70°C (overflow rinsing)

Tank 4 - Tap water rinse at ambient temperature (overflow rinsing).

The samples were then heat dried in the pad steam range at 150°C for 6 minutes. The pectin is measured by staining with ruthenium red dye (standard Ruthenium staining procedure EUS-SM-103) and the data transformed in to the amount of pectin remaining on cloth (% Residual Pectin, see Table III). The data shown in Table III below clearly indicates that the pectate lyase variants of the invention perform better at lower dosages than the wild-type (parent, native) pectate lyase. In contrast, maximum average pectin removal observed for pectate lyases in general are 30% and define as an excellent scouring effect on cotton.

TABLE III

Results in APSU/kg cotton

	Dose for 60% Pectin Removal	Dose for 70% Pectin Removal
Variant M169I + F198V	182	531

Variant M169I + F198V + S220V	740	2379
Variant M169I + F198V + D136A	379	1179
Variant M169I + F198V + T55P	658	2392
Wild-Type Pectate Lyase	3117	7792

EXAMPLE 5

Construction, fermentation, purification and characterization of *Bacillus agaradhaerens* pectate lyase variants

The wild-type *Bacillus agaradhaerens* pectate lyase encoded by SEQ ID NO: 18 is expressed in *B. subtilis* from a plasmid denoted pCA207, which is similar to pMB541 (see Materials and Methods) except for the pectate lyase gene now originating from *Bacillus agaradhaerens*. This plasmid contains a fusion of the signal sequence from *B. licheniformis* alpha-amylase and the gene encoding the mature protein of *Bacillus agaradhaerens* pectate lyase (SEQ ID NO: 17, wild-type pectate lyase), the expression of which is directed by the *B. licheniformis* alpha-amylase promoter.

DNA fragments coding for a specific amino acid change were made using the SOE-PCR methods described by Higuchi, R. et al 1988, [Nucleic Acids Research Vol. 16 (15) p.7351-7367]. pCA207 was used as template in the reaction together with the mutagenesis primers and two primers located 5' to the Pst I site and 3' to the Cel II site, respectively. A major part of the pectate lyase gene was removed from plasmid pCA207 by digestion with the restriction enzymes Pst I and Cel II.

To obtain conjugated and pectate lyase expressing plasmids a PCR based multimerization reaction was made as described by Shafikhani, S. et al., 1997 [BioTechniques 23, 304-310]. The resulting PCR products were transformed into a protease-, amylase-, cellulase and pectate lyase-depleted *Bacillus subtilis*

strain pMB1053-1 in order to express the variant enzyme. The sequence pectate lyase gene and variants were confirmed by automatic sequencing.

The *B. agaradhaerens* pectate lyase variant S82I was constructed by the use of the gene specific primers 101450 (SEQ ID NO: 9) and 6034 (SEQ ID NO: 10), and the mutagenic primers Pely174 (SEQ ID NO: 11) and Pely175 (SEQ ID NO: 12) resulting in a 1.4 kb fragment.

The *B. agaradhaerens* pectate lyase variant D93I was constructed by the use of the gene specific primers 101450 and 6034, and the mutagenic primers Pely176 (SEQ ID NO: 13) and Pely177 (SEQ ID NO: 14) resulting in an 1.4 kb fragment.

The *B. agaradhaerens* pectate lyase variant M179I was constructed by the use of the gene specific primers 101450 and 6034, and the mutagenic primers Pely178 (SEQ ID NO: 15) and Pely179 (SEQ ID NO: 16) resulting in an 1.4 kb fragment.

Primer 101450:
5' CATGGTGAACCAAAGTGAAACC 3' (SEQ ID NO: 9)

Primer 6034:
5' GGAAGAAAATATAGGGAAAATGG 3' (SEQ ID NO: 10)

Primer Pely174:
5' GAAATTAAAAACATCATTATTATCGGTGTAG 3' (SEQ ID NO: 11)

Primer Pely175:
5' CTACACCGATAATAATGATGGTTTTAATTTC 3' (SEQ ID NO: 12)

Primer Pely176:
5' CAAATGGAGAGTTCCATGGCATTGGGATAAG3' (SEQ ID NO: 13)

Primer Pely177:
5' CTTATCCCAATGCCATGGAACTCTCCATTTG 3' (SEQ ID NO: 14)

Primer Pely178:
5' CATTGGAAAACTATCCTCGTCGGTCATAC 3' (SEQ ID NO: 15)

Primer Pely179:

5' GTATGACCGACGAGGATAGTTTTCCAATG 3' (SEQ ID NO: 16)

200 ml of shake flask culture fluid were diluted to 500 ml with ion free water and applied to Q-Sepharose (50 ml column equilibrated with 25 mM Tris(hydroxymethyl)amino-methane buffer, pH 8.0). The pure pectate lyase variant was eluted using a NaCl gradient.

The pectate lyase variant gave a single band in SDS-PAGE of 36 kDa.

By using the methods described in Example 1 and 2, the *Bacillus agaradhaerens* pectate lyase variant (numbering relative to SEQ ID NO: 2) of Table IV below was prepared and subjected to DSC (Differential Scanning Calorimetry) at pH 8 using a temperature increase of 1°C per minute. The wild-type *Bacillus agaradhaerens* pectate lyase (SEQ ID NO: 18) has a DSC unfolding temperature of 60.1°C at pH 8.

Table IV

Substitution relative to SEQ ID NO: 2	DSC unfolding temperature (°C) pH 8
S72I	70.4

EXAMPLE 6

Construction, fermentation, purification and characterization of *Bacillus subtilis* pectate lyase variant

By using the methods described in Example 1 and 2, the *Bacillus subtilis* pectate lyase stack variant C199N (numbering relative to SEQ ID NO:2) of Table V below was prepared and subjected to DSC (Differential Scanning Calorimetry) at pH 8 using a temperature increase of 1°C per minute. The wild-type *Bacillus subtilis* pectate lyase (Nasser et al.: Cloning of a pectate lyase from Bacillus subtilis (1993) FEBS 335:319-326, which is hereby incorporated by reference in its entirety) has a DSC unfolding temperature of 61.1°C at pH 8.

Table I

Pectate Lyase Variant	Substitution in position relative to SEQ ID NO:2 [substitution relative to wt *B. subtilis* pectate lyase numbering, FEBS 335:319-326 (1993)]	DSC unfolding temperature (°C) pH 8
	127 [C199N]	61.9

EXAMPLE 7

Determination of stack positions in *Bacillus licheniformis* pectate lyase

Stack positions in the pectate lyase prepared in example 1 and 2 were determined based on the following rules:

(i) the residue is part of a β-sheet - according to the output of the DSSP program and

(ii) the β-strand is part of a sheet composed of more than two β-strands

OR

(iii) the residue is without secondary structure but is linking two β-sheet regions horizontally

(iv) or the residue is part of a T2 turn composed by no more than two amino acid residues

(v) or the residue has a Cα-atom in line with an already determined stack (i.e. visually it is clearly part of the stack)

Results:

3. In: V24, I47, I73, I97, V124, F155, F183, I205, I228, V253

2. Out: T23, K46, S72, I96, W123, T154, T182, H204, R227, H252

1. In: Q22, L45, V71, I95, I122, I153, I181, G203, I226, W251

17. Out: N70, N94, N121, Y152, T180, E202, R225, Y250

16. Out: S69, N93, K120, E151

18. Out: V68, A92, S119, A150

15. Out: K66, W90, E116, K147

14. In: V65, I89, I115, V146, M169, F198, S220

13. Out: D64, K88, G114, D145, L168, S197, N219, V241

12. In: I63, I87, I113, F144, M167, P196, I218, I240

11. In: G163, L191, I213, A236, S261

10. Out: E104, - , D162, N190, K212, N235, N260

9. Out: T54, K83, H103, Y130, H161, E189, N211, E234, V259

8. In: I53, L82, I102, L129, V160, F188, F210, F233, F258

7. Out: T52, E81, K101, E128, Y159, W187, Y209, L232, K257

6. In: L100, N127, N158, N186, N208, N231, N256

5. Out: N99, H126, W157, H185, N207, N230, N255

4. Out: T25, Y48, V74, R98, D125, S156, H184, Y206, E229, S254

The underlined residues are conserved residues believed to be part of the active site - these would not be chosen for optimisation.

The majority of the residues are classified as stack residues based on rule a.

M167 and P196 are classified according to rule c.

S261, E104, N260, and T54 are classified according to rule e.

Stacks #5 and #6 are classified according to rule d.

Some residues are β-strand residues may no t be regarded as stack-residues: 26, 49, 67, 75, 91, 164, 165, 192, 193, 199, and 221.

The sequence below depicts the stacks - placed such that the stack residues are on top of each other; the stacks are numbered according to the list above.

```
        ADFSLKGFAALNGGTTGGEGGQ

 2 4 6        8 10               1315          17
1 3 5        7 9 11             1214  18      16
-TVT--VTTGDQ-------LIAA-----------L----KNKNANTP
LKIY--VNG----TIT---TSNTSASK------IDVK-DV----------SN
VSIV--GSGTKG-ELK----GIG----------IKIW-RA----------NN
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IIIRNL-------KIHE--VASGDKDA------IGIEGPS----------KN
IWVDHN-------ELY---HSLNVDKDYYDGL-FDVKRDA----------EY
ITFSWN-------YVHDG-WKS-----------MLM----GSSDSDNYNR-T
ITFHHN-------WFENL-NSRV----------PSF----RFG--------E
GHIYNN-------YFNKI-IDSG----------INS----RMGA-------R
IRIENN-------LFENA-KDP-----------I------VSWYSSSPGY
WHVSNN-------KFVNS-RGSMP----------------TT

STTTYNPPYSYSLDNVDNVKSIVKQNAGVGKINP
```

APPENDIX 1

The structural coordinates of the three-dimensional structure of the *Bacillus licheniformis* pectate lyase enzyme

The structural coordinates of the three-dimensional structure of the *Bacillus licheniformis* pectate lyase enzyme (EC 4.2.2.2) as determined by X-ray crystallography. The format of the coordinates is the conventional PDB format (*Protein Data Bank*):

ATOM	1	CB	ALA	A	1	4.950	-3.535	41.947	1.00	29.97	A
ATOM	2	C	ALA	A	1	7.141	-3.311	40.732	1.00	28.81	A
ATOM	3	O	ALA	A	1	8.284	-3.564	41.107	1.00	25.91	A
ATOM	4	N	ALA	A	1	6.466	-5.476	41.726	1.00	25.62	A
ATOM	5	CA	ALA	A	1	5.973	-4.245	41.053	1.00	29.08	A
ATOM	6	N	ASP	A	2	6.839	-2.228	40.029	1.00	27.94	A
ATOM	7	CA	ASP	A	2	7.851	-1.247	39.651	1.00	27.25	A
ATOM	8	CB	ASP	A	2	7.260	-.284	38.628	1.00	28.70	A
ATOM	9	CG	ASP	A	2	8.290	.658	38.052	1.00	34.49	A
ATOM	10	OD1	ASP	A	2	9.438	.686	38.546	1.00	33.41	A
ATOM	11	OD2	ASP	A	2	7.936	1.375	37.096	1.00	32.96	A
ATOM	12	C	ASP	A	2	8.333	-.463	40.869	1.00	23.10	A
ATOM	13	O	ASP	A	2	7.601	.359	41.409	1.00	27.55	A
ATOM	14	N	PHE	A	3	9.560	-.718	41.296	1.00	20.68	A
ATOM	15	CA	PHE	A	3	10.112	-.025	42.447	1.00	23.98	A
ATOM	16	CB	PHE	A	3	10.730	-1.037	43.413	1.00	27.89	A
ATOM	17	CG	PHE	A	3	9.753	-2.053	43.937	1.00	27.46	A
ATOM	18	CD1	PHE	A	3	8.453	-1.686	44.272	1.00	26.88	A
ATOM	19	CD2	PHE	A	3	10.145	-3.373	44.130	1.00	36.04	A
ATOM	20	CE1	PHE	A	3	7.557	-2.612	44.793	1.00	29.43	A
ATOM	21	CE2	PHE	A	3	9.252	-4.319	44.656	1.00	37.79	A
ATOM	22	CZ	PHE	A	3	7.959	-3.934	44.987	1.00	34.66	A
ATOM	23	C	PHE	A	3	11.145	1.058	42.107	1.00	26.95	A
ATOM	24	O	PHE	A	3	11.914	1.483	42.974	1.00	26.06	A
ATOM	25	N	SER	A	4	11.170	1.503	40.855	1.00	23.64	A
ATOM	26	CA	SER	A	4	12.110	2.541	40.460	1.00	26.91	A
ATOM	27	CB	SER	A	4	12.250	2.582	38.935	1.00	27.90	A
ATOM	28	OG	SER	A	4	11.015	2.874	38.318	1.00	28.45	A
ATOM	29	C	SER	A	4	11.648	3.900	40.979	1.00	25.84	A
ATOM	30	O	SER	A	4	10.485	4.078	41.335	1.00	24.99	A
ATOM	31	N	LEU	A	5	12.573	4.851	41.026	1.00	23.85	A
ATOM	32	CA	LEU	A	5	12.287	6.196	41.504	1.00	23.44	A
ATOM	33	CB	LEU	A	5	13.589	6.998	41.608	1.00	28.44	A
ATOM	34	CG	LEU	A	5	13.476	8.471	42.016	1.00	27.22	A
ATOM	35	CD1	LEU	A	5	12.901	8.577	43.410	1.00	27.74	A
ATOM	36	CD2	LEU	A	5	14.841	9.115	41.956	1.00	30.88	A
ATOM	37	C	LEU	A	5	11.311	6.945	40.604	1.00	21.27	A
ATOM	38	O	LEU	A	5	11.503	7.015	39.396	1.00	23.47	A
ATOM	39	N	LYS	A	6	10.269	7.502	41.210	1.00	18.82	A
ATOM	40	CA	LYS	A	6	9.262	8.276	40.495	1.00	19.23	A
ATOM	41	CB	LYS	A	6	7.908	7.555	40.503	1.00	21.65	A
ATOM	42	CG	LYS	A	6	7.917	6.117	40.026	1.00	25.78	A
ATOM	43	CD	LYS	A	6	8.222	6.015	38.549	1.00	32.24	A
ATOM	44	CE	LYS	A	6	8.053	4.583	38.078	1.00	37.55	A
ATOM	45	NZ	LYS	A	6	8.373	4.429	36.622	1.00	44.03	A
ATOM	46	C	LYS	A	6	9.085	9.598	41.243	1.00	22.99	A
ATOM	47	O	LYS	A	6	9.458	9.707	42.412	1.00	21.67	A
ATOM	48	N	GLY	A	7	8.522	10.592	40.563	1.00	19.72	A
ATOM	49	CA	GLY	A	7	8.243	11.861	41.201	1.00	22.73	A
ATOM	50	C	GLY	A	7	9.320	12.912	41.293	1.00	26.23	A
ATOM	51	O	GLY	A	7	10.365	12.825	40.648	1.00	26.17	A
ATOM	52	N	PHE	A	8	9.042	13.902	42.133	1.00	24.93	A
ATOM	53	CA	PHE	A	8	9.915	15.047	42.347	1.00	24.97	A
ATOM	54	CB	PHE	A	8	9.328	15.946	43.438	1.00	24.71	A
ATOM	55	CG	PHE	A	8	8.171	16.786	42.978	1.00	22.82	A
ATOM	56	CD1	PHE	A	8	6.896	16.589	43.500	1.00	20.85	A
ATOM	57	CD2	PHE	A	8	8.364	17.803	42.040	1.00	24.14	A

ATOM	58	CE1	PHE	A	8	5.827	17.392	43.099	1.00	26.19	A
ATOM	59	CE2	PHE	A	8	7.302	18.610	41.634	1.00	23.90	A
ATOM	60	CZ	PHE	A	8	6.028	18.402	42.168	1.00	24.17	A
ATOM	61	C	PHE	A	8	11.381	14.765	42.658	1.00	25.06	A
ATOM	62	O	PHE	A	8	12.240	15.571	42.301	1.00	28.48	A
ATOM	63	N	ALA	A	9	11.683	13.647	43.316	1.00	21.01	A
ATOM	64	CA	ALA	A	9	13.079	13.341	43.639	1.00	23.79	A
ATOM	65	CB	ALA	A	9	13.152	12.296	44.739	1.00	21.26	A
ATOM	66	C	ALA	A	9	13.861	12.869	42.403	1.00	26.51	A
ATOM	67	O	ALA	A	9	15.089	12.751	42.434	1.00	27.92	A
ATOM	68	N	ALA	A	10	13.144	12.598	41.318	1.00	24.45	A
ATOM	69	CA	ALA	A	10	13.769	12.169	40.080	1.00	27.35	A
ATOM	70	CB	ALA	A	10	12.810	11.304	39.283	1.00	27.35	A
ATOM	71	C	ALA	A	10	14.188	13.373	39.246	1.00	30.00	A
ATOM	72	O	ALA	A	10	14.885	13.221	38.242	1.00	31.02	A
ATOM	73	N	LEU	A	11	13.760	14.563	39.659	1.00	27.87	A
ATOM	74	CA	LEU	A	11	14.084	15.789	38.941	1.00	31.90	A
ATOM	75	CB	LEU	A	11	12.915	16.772	39.015	1.00	26.46	A
ATOM	76	CG	LEU	A	11	11.592	16.322	38.411	1.00	29.00	A
ATOM	77	CD1	LEU	A	11	10.559	17.429	38.574	1.00	31.30	A
ATOM	78	CD2	LEU	A	11	11.793	15.980	36.944	1.00	33.67	A
ATOM	79	C	LEU	A	11	15.321	16.465	39.510	1.00	37.10	A
ATOM	80	O	LEU	A	11	15.914	16.001	40.493	1.00	37.78	A
ATOM	81	N	ASN	A	12	15.704	17.565	38.869	1.00	39.12	A
ATOM	82	CA	ASN	A	12	16.846	18.353	39.302	1.00	40.01	A
ATOM	83	CB	ASN	A	12	16.512	19.054	40.622	1.00	42.90	A
ATOM	84	CG	ASN	A	12	17.503	20.143	40.964	1.00	47.96	A
ATOM	85	OD1	ASN	A	12	18.297	20.014	41.906	1.00	47.98	A
ATOM	86	ND2	ASN	A	12	17.470	21.227	40.191	1.00	45.22	A
ATOM	87	C	ASN	A	12	18.086	17.494	39.478	1.00	39.53	A
ATOM	88	O	ASN	A	12	18.859	17.679	40.419	1.00	42.10	A
ATOM	89	N	GLY	A	13	18.266	16.542	38.579	1.00	38.17	A
ATOM	90	CA	GLY	A	13	19.430	15.682	38.658	1.00	36.46	A
ATOM	91	C	GLY	A	13	19.170	14.279	39.173	1.00	38.00	A
ATOM	92	O	GLY	A	13	20.025	13.408	39.049	1.00	38.23	A
ATOM	93	N	GLY	A	14	18.001	14.049	39.761	1.00	38.16	A
ATOM	94	CA	GLY	A	14	17.685	12.724	40.266	1.00	31.19	A
ATOM	95	C	GLY	A	14	18.250	12.453	41.642	1.00	31.71	A
ATOM	96	O	GLY	A	14	18.946	13.283	42.222	1.00	32.16	A
ATOM	97	N	THR	A	15	17.945	11.277	42.178	1.00	31.26	A
ATOM	98	CA	THR	A	15	18.423	10.908	43.500	1.00	28.08	A
ATOM	99	CB	THR	A	15	17.276	10.955	44.530	1.00	26.89	A
ATOM	100	OG1	THR	A	15	16.766	12.290	44.609	1.00	26.05	A
ATOM	101	CG2	THR	A	15	17.762	10.534	45.899	1.00	23.93	A
ATOM	102	C	THR	A	15	19.016	9.510	43.465	1.00	30.83	A
ATOM	103	O	THR	A	15	18.324	8.541	43.163	1.00	32.55	A
ATOM	104	N	THR	A	16	20.304	9.408	43.764	1.00	29.74	A
ATOM	105	CA	THR	A	16	20.974	8.116	43.766	1.00	32.12	A
ATOM	106	CB	THR	A	16	22.107	8.074	42.734	1.00	33.40	A
ATOM	107	OG1	THR	A	16	23.101	9.042	43.074	1.00	34.75	A
ATOM	108	CG2	THR	A	16	21.573	8.383	41.350	1.00	34.80	A
ATOM	109	C	THR	A	16	21.554	7.813	45.143	1.00	33.25	A
ATOM	110	O	THR	A	16	22.132	6.749	45.365	1.00	33.52	A
ATOM	111	N	GLY	A	17	21.406	8.760	46.063	1.00	32.25	A
ATOM	112	CA	GLY	A	17	21.902	8.556	47.413	1.00	32.17	A
ATOM	113	C	GLY	A	17	23.382	8.216	47.485	1.00	37.71	A
ATOM	114	O	GLY	A	17	24.209	8.888	46.867	1.00	34.80	A
ATOM	115	N	GLY	A	18	23.721	7.162	48.223	1.00	36.58	A
ATOM	116	CA	GLY	A	18	25.120	6.792	48.362	1.00	38.84	A
ATOM	117	C	GLY	A	18	25.565	5.650	47.480	1.00	41.94	A
ATOM	118	O	GLY	A	18	26.571	4.997	47.752	1.00	41.09	A
ATOM	119	N	GLU	A	19	24.824	5.417	46.409	1.00	42.19	A
ATOM	120	CA	GLU	A	19	25.141	4.336	45.499	1.00	46.48	A
ATOM	121	CB	GLU	A	19	23.981	4.142	44.519	1.00	44.81	A
ATOM	122	CG	GLU	A	19	23.918	2.774	43.877	1.00	51.26	A
ATOM	123	CD	GLU	A	19	23.361	1.704	44.802	1.00	51.51	A
ATOM	124	OE1	GLU	A	19	23.344	.525	44.393	1.00	56.08	A
ATOM	125	OE2	GLU	A	19	22.935	2.036	45.928	1.00	48.34	A
ATOM	126	C	GLU	A	19	26.425	4.673	44.742	1.00	48.73	A

ATOM	127	O	GLU	A	19	26.686	5.835	44.422	1.00	49.43	A
ATOM	128	N	GLY	A	20	27.237	3.656	44.473	1.00	51.06	A
ATOM	129	CA	GLY	A	20	28.467	3.875	43.729	1.00	51.44	A
ATOM	130	C	GLY	A	20	29.649	4.388	44.531	1.00	52.89	A
ATOM	131	O	GLY	A	20	30.580	4.977	43.969	1.00	53.13	A
ATOM	132	N	GLY	A	21	29.629	4.163	45.842	1.00	53.37	A
ATOM	133	CA	GLY	A	21	30.725	4.630	46.675	1.00	52.96	A
ATOM	134	C	GLY	A	21	31.136	3.604	47.710	1.00	54.35	A
ATOM	135	O	GLY	A	21	31.163	2.401	47.437	1.00	53.00	A
ATOM	136	N	GLN	A	22	31.444	4.075	48.913	1.00	54.59	A
ATOM	137	CA	GLN	A	22	31.855	3.179	49.976	1.00	56.12	A
ATOM	138	CB	GLN	A	22	32.676	3.944	51.016	1.00	60.58	A
ATOM	139	CG	GLN	A	22	33.929	4.570	50.445	1.00	66.25	A
ATOM	140	CD	GLN	A	22	34.930	4.923	51.524	1.00	71.32	A
ATOM	141	OE1	GLN	A	22	34.649	5.743	52.407	1.00	73.61	A
ATOM	142	NE2	GLN	A	22	36.107	4.299	51.466	1.00	72.09	A
ATOM	143	C	GLN	A	22	30.657	2.535	50.640	1.00	54.61	A
ATOM	144	O	GLN	A	22	29.536	3.042	50.559	1.00	55.56	A
ATOM	145	N	THR	A	23	30.896	1.413	51.305	1.00	51.09	A
ATOM	146	CA	THR	A	23	29.826	.710	51.985	1.00	51.15	A
ATOM	147	CB	THR	A	23	29.452	-.573	51.251	1.00	49.07	A
ATOM	148	OG1	THR	A	23	28.963	-.249	49.943	1.00	49.98	A
ATOM	149	CG2	THR	A	23	28.380	-1.327	52.028	1.00	51.23	A
ATOM	150	C	THR	A	23	30.242	.341	53.393	1.00	51.40	A
ATOM	151	O	THR	A	23	31.332	-.184	53.601	1.00	53.27	A
ATOM	152	N	VAL	A	24	29.372	.618	54.358	1.00	50.47	A
ATOM	153	CA	VAL	A	24	29.646	.294	55.751	1.00	49.72	A
ATOM	154	CB	VAL	A	24	29.990	1.555	56.562	1.00	48.78	A
ATOM	155	CG1	VAL	A	24	30.517	1.163	57.934	1.00	51.52	A
ATOM	156	CG2	VAL	A	24	31.020	2.378	55.819	1.00	51.60	A
ATOM	157	C	VAL	A	24	28.414	-.347	56.368	1.00	50.01	A
ATOM	158	O	VAL	A	24	27.288	-.058	55.963	1.00	50.75	A
ATOM	159	N	THR	A	25	28.631	-1.233	57.335	1.00	47.67	A
ATOM	160	CA	THR	A	25	27.537	-1.891	58.032	1.00	44.98	A
ATOM	161	CB	THR	A	25	27.620	-3.412	57.882	1.00	47.73	A
ATOM	162	OG1	THR	A	25	27.585	-3.762	56.488	1.00	45.97	A
ATOM	163	CG2	THR	A	25	26.456	-4.075	58.602	1.00	46.06	A
ATOM	164	C	THR	A	25	27.668	-1.526	59.506	1.00	47.92	A
ATOM	165	O	THR	A	25	28.757	-1.630	60.083	1.00	47.02	A
ATOM	166	N	VAL	A	26	26.562	-1.098	60.117	1.00	46.57	A
ATOM	167	CA	VAL	A	26	26.581	-.703	61.518	1.00	44.63	A
ATOM	168	CB	VAL	A	26	26.300	.807	61.674	1.00	46.66	A
ATOM	169	CG1	VAL	A	26	27.324	1.607	60.877	1.00	43.61	A
ATOM	170	CG2	VAL	A	26	24.877	1.123	61.196	1.00	45.46	A
ATOM	171	C	VAL	A	26	25.543	-1.470	62.307	1.00	46.12	A
ATOM	172	O	VAL	A	26	24.608	-2.024	61.732	1.00	48.77	A
ATOM	173	N	THR	A	27	25.706	-1.499	63.630	1.00	45.85	A
ATOM	174	CA	THR	A	27	24.768	-2.206	64.487	1.00	43.88	A
ATOM	175	CB	THR	A	27	25.387	-3.514	65.016	1.00	47.14	A
ATOM	176	OG1	THR	A	27	26.538	-3.207	65.815	1.00	52.74	A
ATOM	177	CG2	THR	A	27	25.819	-4.403	63.854	1.00	43.71	A
ATOM	178	C	THR	A	27	24.329	-1.346	65.665	1.00	43.87	A
ATOM	179	O	THR	A	27	23.481	-1.751	66.460	1.00	44.54	A
ATOM	180	N	THR	A	28	24.892	-.148	65.778	1.00	43.72	A
ATOM	181	CA	THR	A	28	24.506	.739	66.877	1.00	45.42	A
ATOM	182	CB	THR	A	28	25.552	.752	67.996	1.00	44.72	A
ATOM	183	OG1	THR	A	28	26.720	1.437	67.531	1.00	45.92	A
ATOM	184	CG2	THR	A	28	25.924	-.669	68.404	1.00	46.14	A
ATOM	185	C	THR	A	28	24.365	2.169	66.395	1.00	44.36	A
ATOM	186	O	THR	A	28	24.907	2.538	65.355	1.00	44.85	A
ATOM	187	N	GLY	A	29	23.642	2.979	67.158	1.00	46.41	A
ATOM	188	CA	GLY	A	29	23.481	4.369	66.773	1.00	45.13	A
ATOM	189	C	GLY	A	29	24.824	5.071	66.729	1.00	46.40	A
ATOM	190	O	GLY	A	29	25.094	5.866	65.822	1.00	50.01	A
ATOM	191	N	ASP	A	30	25.683	4.772	67.701	1.00	46.78	A
ATOM	192	CA	ASP	A	30	26.997	5.404	67.760	1.00	47.64	A
ATOM	193	CB	ASP	A	30	27.709	5.029	69.067	1.00	50.07	A
ATOM	194	CG	ASP	A	30	27.211	5.846	70.250	1.00	51.81	A
ATOM	195	OD1	ASP	A	30	27.492	5.463	71.411	1.00	53.53	A

ATOM	196	OD2	ASP	A	30	26.547	6.881	70.012	1.00	52.51	A
ATOM	197	C	ASP	A	30	27.870	5.073	66.565	1.00	47.34	A
ATOM	198	O	ASP	A	30	28.645	5.916	66.108	1.00	52.03	A
ATOM	199	N	GLN	A	31	27.769	3.853	66.052	1.00	46.12	A
ATOM	200	CA	GLN	A	31	28.573	3.501	64.885	1.00	47.60	A
ATOM	201	CB	GLN	A	31	28.524	1.996	64.621	1.00	47.01	A
ATOM	202	CG	GLN	A	31	28.945	1.162	65.808	1.00	50.99	A
ATOM	203	CD	GLN	A	31	29.018	-.307	65.483	1.00	51.55	A
ATOM	204	OE1	GLN	A	31	28.319	-.795	64.587	1.00	52.47	A
ATOM	205	NE2	GLN	A	31	29.850	-1.033	66.220	1.00	54.27	A
ATOM	206	C	GLN	A	31	28.025	4.255	63.676	1.00	46.55	A
ATOM	207	O	GLN	A	31	28.787	4.744	62.832	1.00	47.12	A
ATOM	208	N	LEU	A	32	26.699	4.350	63.598	1.00	45.46	A
ATOM	209	CA	LEU	A	32	26.048	5.053	62.496	1.00	42.05	A
ATOM	210	CB	LEU	A	32	24.521	4.922	62.635	1.00	40.02	A
ATOM	211	CG	LEU	A	32	23.563	5.634	61.667	1.00	42.52	A
ATOM	212	CD1	LEU	A	32	24.026	5.485	60.222	1.00	38.27	A
ATOM	213	CD2	LEU	A	32	22.171	5.044	61.844	1.00	37.87	A
ATOM	214	C	LEU	A	32	26.487	6.524	62.497	1.00	42.82	A
ATOM	215	O	LEU	A	32	26.905	7.063	61.467	1.00	45.16	A
ATOM	216	N	ILE	A	33	26.410	7.170	63.654	1.00	43.95	A
ATOM	217	CA	ILE	A	33	26.826	8.565	63.752	1.00	42.81	A
ATOM	218	CB	ILE	A	33	26.627	9.081	65.183	1.00	44.86	A
ATOM	219	CG2	ILE	A	33	27.337	10.417	65.375	1.00	46.69	A
ATOM	220	CG1	ILE	A	33	25.131	9.219	65.464	1.00	43.22	A
ATOM	221	CD1	ILE	A	33	24.810	9.624	66.895	1.00	49.50	A
ATOM	222	C	ILE	A	33	28.293	8.703	63.340	1.00	44.54	A
ATOM	223	O	ILE	A	33	28.669	9.638	62.625	1.00	43.81	A
ATOM	224	N	ALA	A	34	29.118	7.755	63.776	1.00	45.26	A
ATOM	225	CA	ALA	A	34	30.546	7.762	63.448	1.00	45.68	A
ATOM	226	CB	ALA	A	34	31.241	6.590	64.140	1.00	44.39	A
ATOM	227	C	ALA	A	34	30.779	7.681	61.941	1.00	46.92	A
ATOM	228	O	ALA	A	34	31.615	8.408	61.383	1.00	49.62	A
ATOM	229	N	ALA	A	35	30.042	6.792	61.278	1.00	46.19	A
ATOM	230	CA	ALA	A	35	30.173	6.628	59.833	1.00	44.81	A
ATOM	231	CB	ALA	A	35	29.287	5.477	59.349	1.00	41.18	A
ATOM	232	C	ALA	A	35	29.819	7.920	59.093	1.00	44.98	A
ATOM	233	O	ALA	A	35	30.471	8.275	58.110	1.00	46.04	A
ATOM	234	N	LEU	A	36	28.789	8.626	59.556	1.00	45.72	A
ATOM	235	CA	LEU	A	36	28.390	9.870	58.907	1.00	43.97	A
ATOM	236	CB	LEU	A	36	27.030	10.345	59.443	1.00	44.00	A
ATOM	237	CG	LEU	A	36	25.813	9.504	59.024	1.00	40.34	A
ATOM	238	CD1	LEU	A	36	24.575	9.975	59.747	1.00	38.08	A
ATOM	239	CD2	LEU	A	36	25.613	9.606	57.520	1.00	41.95	A
ATOM	240	C	LEU	A	36	29.453	10.955	59.083	1.00	48.11	A
ATOM	241	O	LEU	A	36	29.692	11.750	58.170	1.00	46.52	A
ATOM	242	N	LYS	A	37	30.113	10.996	60.238	1.00	52.73	A
ATOM	243	CA	LYS	A	37	31.163	12.004	60.444	1.00	57.77	A
ATOM	244	CB	LYS	A	37	31.556	12.086	61.919	1.00	61.02	A
ATOM	245	CG	LYS	A	37	30.494	12.714	62.802	1.00	63.63	A
ATOM	246	CD	LYS	A	37	31.036	12.981	64.194	1.00	68.53	A
ATOM	247	CE	LYS	A	37	29.929	13.503	65.104	1.00	72.52	A
ATOM	248	NZ	LYS	A	37	29.253	14.681	64.492	1.00	75.63	A
ATOM	249	C	LYS	A	37	32.415	11.694	59.626	1.00	59.17	A
ATOM	250	O	LYS	A	37	33.058	12.587	59.060	1.00	58.21	A
ATOM	251	N	ASN	A	38	32.761	10.417	59.564	1.00	60.90	A
ATOM	252	CA	ASN	A	38	33.943	9.994	58.827	1.00	62.24	A
ATOM	253	CB	ASN	A	38	34.367	8.596	59.288	1.00	66.96	A
ATOM	254	CG	ASN	A	38	34.811	8.576	60.741	1.00	71.22	A
ATOM	255	OD1	ASN	A	38	35.719	9.318	61.130	1.00	71.67	A
ATOM	256	ND2	ASN	A	38	34.175	7.724	61.555	1.00	73.20	A
ATOM	257	C	ASN	A	38	33.739	9.984	57.323	1.00	60.21	A
ATOM	258	O	ASN	A	38	34.612	9.520	56.587	1.00	60.45	A
ATOM	259	N	LYS	A	39	32.613	10.511	56.849	1.00	55.40	A
ATOM	260	CA	LYS	A	39	32.371	10.480	55.416	1.00	53.53	A
ATOM	261	CB	LYS	A	39	30.925	10.857	55.075	1.00	51.04	A
ATOM	262	CG	LYS	A	39	30.671	10.796	53.574	1.00	47.45	A
ATOM	263	CD	LYS	A	39	29.269	11.240	53.189	1.00	46.57	A
ATOM	264	CE	LYS	A	39	29.066	11.123	51.687	1.00	41.37	A

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ATOM    265  NZ  LYS A  39      29.949  12.033  50.918  1.00 42.16      A
ATOM    266  C   LYS A  39      33.292  11.361  54.592  1.00 54.83      A
ATOM    267  O   LYS A  39      33.509  12.525  54.908  1.00 53.37      A
ATOM    268  N   ASN A  40      33.815  10.793  53.513  1.00 58.66      A
ATOM    269  CA  ASN A  40      34.691  11.507  52.603  1.00 62.28      A
ATOM    270  CB  ASN A  40      35.517  10.491  51.800  1.00 68.87      A
ATOM    271  CG  ASN A  40      36.461  11.147  50.798  1.00 76.71      A
ATOM    272  OD1 ASN A  40      37.108  12.165  51.094  1.00 79.61      A
ATOM    273  ND2 ASN A  40      36.562  10.550  49.604  1.00 80.36      A
ATOM    274  C   ASN A  40      33.737  12.288  51.702  1.00 62.09      A
ATOM    275  O   ASN A  40      32.914  11.692  50.981  1.00 62.39      A
ATOM    276  N   ALA A  41      33.837  13.616  51.754  1.00 56.18      A
ATOM    277  CA  ALA A  41      32.961  14.486  50.974  1.00 56.09      A
ATOM    278  CB  ALA A  41      33.351  15.944  51.185  1.00 53.10      A
ATOM    279  C   ALA A  41      32.930  14.185  49.488  1.00 54.78      A
ATOM    280  O   ALA A  41      31.971  14.535  48.792  1.00 55.02      A
ATOM    281  N   ASN A  42      33.968  13.523  49.002  1.00 56.07      A
ATOM    282  CA  ASN A  42      34.077  13.215  47.578  1.00 56.37      A
ATOM    283  CB  ASN A  42      35.518  13.412  47.146  1.00 61.10      A
ATOM    284  CG  ASN A  42      35.917  14.852  47.181  1.00 67.74      A
ATOM    285  OD1 ASN A  42      35.707  15.587  46.206  1.00 70.38      A
ATOM    286  ND2 ASN A  42      36.467  15.293  48.317  1.00 69.40      A
ATOM    287  C   ASN A  42      33.629  11.826  47.190  1.00 53.20      A
ATOM    288  O   ASN A  42      33.672  11.463  46.015  1.00 53.84      A
ATOM    289  N   THR A  43      33.202  11.051  48.172  1.00 49.53      A
ATOM    290  CA  THR A  43      32.763   9.700  47.900  1.00 51.31      A
ATOM    291  CB  THR A  43      33.774   8.678  48.474  1.00 52.31      A
ATOM    292  OG1 THR A  43      35.024   8.806  47.783  1.00 55.41      A
ATOM    293  CG2 THR A  43      33.266   7.256  48.303  1.00 54.61      A
ATOM    294  C   THR A  43      31.381   9.414  48.470  1.00 49.73      A
ATOM    295  O   THR A  43      31.088   9.749  49.621  1.00 49.54      A
ATOM    296  N   PRO A  44      30.498   8.827  47.647  1.00 48.23      A
ATOM    297  CD  PRO A  44      30.645   8.661  46.189  1.00 46.76      A
ATOM    298  CA  PRO A  44      29.141   8.483  48.079  1.00 45.77      A
ATOM    299  CB  PRO A  44      28.527   7.880  46.819  1.00 45.61      A
ATOM    300  CG  PRO A  44      29.205   8.674  45.719  1.00 46.63      A
ATOM    301  C   PRO A  44      29.286   7.449  49.193  1.00 43.06      A
ATOM    302  O   PRO A  44      30.208   6.634  49.164  1.00 41.74      A
ATOM    303  N   LEU A  45      28.390   7.479  50.172  1.00 42.54      A
ATOM    304  CA  LEU A  45      28.456   6.520  51.264  1.00 37.62      A
ATOM    305  CB  LEU A  45      28.812   7.242  52.567  1.00 34.48      A
ATOM    306  CG  LEU A  45      28.844   6.371  53.829  1.00 37.59      A
ATOM    307  CD1 LEU A  45      29.987   5.353  53.736  1.00 38.60      A
ATOM    308  CD2 LEU A  45      29.009   7.258  55.051  1.00 37.86      A
ATOM    309  C   LEU A  45      27.140   5.756  51.425  1.00 38.36      A
ATOM    310  O   LEU A  45      26.063   6.354  51.469  1.00 38.38      A
ATOM    311  N   LYS A  46      27.232   4.432  51.494  1.00 36.30      A
ATOM    312  CA  LYS A  46      26.058   3.592  51.672  1.00 36.57      A
ATOM    313  CB  LYS A  46      25.934   2.583  50.531  1.00 35.15      A
ATOM    314  CG  LYS A  46      24.678   1.732  50.596  1.00 38.66      A
ATOM    315  CD  LYS A  46      24.522    .925  49.324  1.00 43.86      A
ATOM    316  CE  LYS A  46      23.250    .104  49.329  1.00 44.29      A
ATOM    317  NZ  LYS A  46      23.085   -.595  48.014  1.00 48.16      A
ATOM    318  C   LYS A  46      26.240   2.875  52.993  1.00 36.60      A
ATOM    319  O   LYS A  46      27.216   2.154  53.194  1.00 40.17      A
ATOM    320  N   ILE A  47      25.292   3.079  53.894  1.00 38.76      A
ATOM    321  CA  ILE A  47      25.350   2.496  55.225  1.00 38.45      A
ATOM    322  CB  ILE A  47      25.195   3.606  56.283  1.00 36.85      A
ATOM    323  CG2 ILE A  47      25.331   3.026  57.673  1.00 40.36      A
ATOM    324  CG1 ILE A  47      26.239   4.704  56.041  1.00 39.18      A
ATOM    325  CD1 ILE A  47      26.038   5.956  56.896  1.00 37.69      A
ATOM    326  C   ILE A  47      24.245   1.460  55.430  1.00 42.76      A
ATOM    327  O   ILE A  47      23.065   1.760  55.237  1.00 43.75      A
ATOM    328  N   TYR A  48      24.631    .240  55.805  1.00 42.07      A
ATOM    329  CA  TYR A  48      23.660   -.821  56.070  1.00 41.82      A
ATOM    330  CB  TYR A  48      24.160  -2.177  55.576  1.00 42.57      A
ATOM    331  CG  TYR A  48      24.069  -2.370  54.087  1.00 42.53      A
ATOM    332  CD1 TYR A  48      25.107  -1.970  53.247  1.00 43.49      A
ATOM    333  CE1 TYR A  48      25.022  -2.152  51.862  1.00 45.34      A
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ATOM    334  CD2 TYR A  48      22.938  -2.954  53.514  1.00 42.25      A
ATOM    335  CE2 TYR A  48      22.842  -3.139  52.133  1.00 42.26      A
ATOM    336  CZ  TYR A  48      23.884  -2.737  51.318  1.00 42.33      A
ATOM    337  OH  TYR A  48      23.781  -2.911  49.963  1.00 47.07      A
ATOM    338  C   TYR A  48      23.435   -.923  57.563  1.00 43.39      A
ATOM    339  O   TYR A  48      24.393   -.999  58.334  1.00 45.87      A
ATOM    340  N   VAL A  49      22.175   -.916  57.978  1.00 41.74      A
ATOM    341  CA  VAL A  49      21.865  -1.029  59.389  1.00 41.59      A
ATOM    342  CB  VAL A  49      20.717   -.092  59.789  1.00 39.00      A
ATOM    343  CG1 VAL A  49      20.329   -.338  61.248  1.00 38.57      A
ATOM    344  CG2 VAL A  49      21.151   1.356  59.598  1.00 38.26      A
ATOM    345  C   VAL A  49      21.484  -2.476  59.648  1.00 44.39      A
ATOM    346  O   VAL A  49      20.400  -2.942  59.258  1.00 41.59      A
ATOM    347  N   ASN A  50      22.390  -3.193  60.304  1.00 47.06      A
ATOM    348  CA  ASN A  50      22.172  -4.600  60.595  1.00 48.99      A
ATOM    349  CB  ASN A  50      23.318  -5.421  60.003  1.00 50.89      A
ATOM    350  CG  ASN A  50      23.021  -6.899  59.984  1.00 56.75      A
ATOM    351  OD1 ASN A  50      21.896  -7.313  59.683  1.00 59.76      A
ATOM    352  ND2 ASN A  50      24.033  -7.716  60.287  1.00 60.71      A
ATOM    353  C   ASN A  50      22.046  -4.863  62.085  1.00 49.06      A
ATOM    354  O   ASN A  50      22.671  -5.779  62.620  1.00 53.82      A
ATOM    355  N   GLY A  51      21.231  -4.054  62.756  1.00 48.71      A
ATOM    356  CA  GLY A  51      21.032  -4.228  64.182  1.00 48.43      A
ATOM    357  C   GLY A  51      19.933  -3.312  64.668  1.00 48.36      A
ATOM    358  O   GLY A  51      19.323  -2.598  63.871  1.00 50.46      A
ATOM    359  N   THR A  52      19.661  -3.326  65.966  1.00 47.31      A
ATOM    360  CA  THR A  52      18.626  -2.463  66.512  1.00 45.90      A
ATOM    361  CB  THR A  52      17.774  -3.205  67.560  1.00 44.26      A
ATOM    362  OG1 THR A  52      17.130  -4.326  66.937  1.00 44.02      A
ATOM    363  CG2 THR A  52      16.712  -2.275  68.146  1.00 44.32      A
ATOM    364  C   THR A  52      19.259  -1.229  67.148  1.00 47.07      A
ATOM    365  O   THR A  52      20.015  -1.328  68.121  1.00 47.56      A
ATOM    366  N   ILE A  53      18.960   -.069  66.570  1.00 45.15      A
ATOM    367  CA  ILE A  53      19.467   1.203  67.062  1.00 44.66      A
ATOM    368  CB  ILE A  53      19.454   2.277  65.964  1.00 42.52      A
ATOM    369  CG2 ILE A  53      20.130   3.537  66.477  1.00 40.37      A
ATOM    370  CG1 ILE A  53      20.121   1.743  64.695  1.00 42.74      A
ATOM    371  CD1 ILE A  53      21.569   1.359  64.855  1.00 45.74      A
ATOM    372  C   ILE A  53      18.530   1.667  68.161  1.00 45.52      A
ATOM    373  O   ILE A  53      17.313   1.703  67.965  1.00 47.42      A
ATOM    374  N   THR A  54      19.089   2.023  69.312  1.00 45.89      A
ATOM    375  CA  THR A  54      18.275   2.481  70.433  1.00 46.53      A
ATOM    376  CB  THR A  54      18.006   1.345  71.432  1.00 46.15      A
ATOM    377  OG1 THR A  54      19.252    .888  71.972  1.00 49.93      A
ATOM    378  CG2 THR A  54      17.315    .180  70.738  1.00 44.89      A
ATOM    379  C   THR A  54      18.964   3.608  71.173  1.00 45.77      A
ATOM    380  O   THR A  54      20.078   4.017  70.820  1.00 44.58      A
ATOM    381  N   THR A  55      18.280   4.123  72.188  1.00 48.39      A
ATOM    382  CA  THR A  55      18.825   5.200  72.997  1.00 51.24      A
ATOM    383  CB  THR A  55      17.747   5.795  73.924  1.00 52.73      A
ATOM    384  OG1 THR A  55      17.064   4.730  74.606  1.00 54.03      A
ATOM    385  CG2 THR A  55      16.734   6.607  73.103  1.00 50.34      A
ATOM    386  C   THR A  55      19.964   4.642  73.837  1.00 52.28      A
ATOM    387  O   THR A  55      20.816   5.395  74.316  1.00 53.84      A
ATOM    388  N   SER A  56      19.975   3.319  74.003  1.00 51.40      A
ATOM    389  CA  SER A  56      21.005   2.628  74.776  1.00 52.14      A
ATOM    390  CB  SER A  56      20.558   1.203  75.112  1.00 50.42      A
ATOM    391  OG  SER A  56      19.521   1.218  76.077  1.00 55.68      A
ATOM    392  C   SER A  56      22.339   2.559  74.046  1.00 52.10      A
ATOM    393  O   SER A  56      23.394   2.563  74.685  1.00 53.73      A
ATOM    394  N   ASN A  57      22.304   2.466  72.716  1.00 49.19      A
ATOM    395  CA  ASN A  57      23.547   2.409  71.952  1.00 47.75      A
ATOM    396  CB  ASN A  57      23.616   1.132  71.106  1.00 43.72      A
ATOM    397  CG  ASN A  57      22.472   1.011  70.114  1.00 44.67      A
ATOM    398  OD1 ASN A  57      22.081   1.987  69.473  1.00 46.77      A
ATOM    399  ND2 ASN A  57      21.948   -.196  69.965  1.00 42.55      A
ATOM    400  C   ASN A  57      23.764   3.639  71.064  1.00 47.69      A
ATOM    401  O   ASN A  57      24.482   3.580  70.063  1.00 49.13      A
ATOM    402  N   THR A  58      23.144   4.754  71.443  1.00 47.99      A
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ATOM    403  CA  THR A  58      23.281   6.008  70.705  1.00 46.33      A
ATOM    404  CB  THR A  58      21.991   6.358  69.933  1.00 46.92      A
ATOM    405  OG1 THR A  58      21.673   5.291  69.035  1.00 46.87      A
ATOM    406  CG2 THR A  58      22.175   7.645  69.138  1.00 45.05      A
ATOM    407  C   THR A  58      23.551   7.117  71.708  1.00 45.30      A
ATOM    408  O   THR A  58      22.745   7.346  72.612  1.00 46.40      A
ATOM    409  N   SER A  59      24.682   7.801  71.542  1.00 46.96      A
ATOM    410  CA  SER A  59      25.076   8.888  72.439  1.00 50.13      A
ATOM    411  CB  SER A  59      26.595   9.079  72.404  1.00 50.34      A
ATOM    412  OG  SER A  59      27.281   7.930  72.884  1.00 54.01      A
ATOM    413  C   SER A  59      24.409  10.223  72.119  1.00 51.76      A
ATOM    414  O   SER A  59      24.771  11.250  72.702  1.00 54.96      A
ATOM    415  N   ALA A  60      23.458  10.223  71.188  1.00 50.03      A
ATOM    416  CA  ALA A  60      22.752  11.451  70.824  1.00 47.22      A
ATOM    417  CB  ALA A  60      23.090  11.844  69.396  1.00 46.88      A
ATOM    418  C   ALA A  60      21.252  11.206  70.971  1.00 48.26      A
ATOM    419  O   ALA A  60      20.814  10.060  71.083  1.00 46.96      A
ATOM    420  N   SER A  61      20.462  12.276  70.980  1.00 47.89      A
ATOM    421  CA  SER A  61      19.019  12.129  71.119  1.00 49.10      A
ATOM    422  CB  SER A  61      18.413  13.429  71.658  1.00 49.82      A
ATOM    423  OG  SER A  61      18.597  14.490  70.734  1.00 54.81      A
ATOM    424  C   SER A  61      18.360  11.752  69.783  1.00 48.17      A
ATOM    425  O   SER A  61      17.168  11.425  69.735  1.00 49.38      A
ATOM    426  N   LYS A  62      19.143  11.798  68.705  1.00 49.22      A
ATOM    427  CA  LYS A  62      18.655  11.448  67.369  1.00 47.57      A
ATOM    428  CB  LYS A  62      17.698  12.532  66.857  1.00 44.52      A
ATOM    429  CG  LYS A  62      18.294  13.925  66.825  1.00 45.13      A
ATOM    430  CD  LYS A  62      17.267  14.947  66.369  1.00 45.99      A
ATOM    431  CE  LYS A  62      17.690  16.361  66.735  1.00 49.54      A
ATOM    432  NZ  LYS A  62      19.042  16.702  66.204  1.00 51.37      A
ATOM    433  C   LYS A  62      19.813  11.270  66.382  1.00 46.37      A
ATOM    434  O   LYS A  62      20.944  11.666  66.663  1.00 46.95      A
ATOM    435  N   ILE A  63      19.529  10.663  65.231  1.00 43.01      A
ATOM    436  CA  ILE A  63      20.547  10.467  64.212  1.00 43.30      A
ATOM    437  CB  ILE A  63      20.311   9.176  63.415  1.00 41.49      A
ATOM    438  CG2 ILE A  63      21.427   8.981  62.415  1.00 43.26      A
ATOM    439  CG1 ILE A  63      20.242   7.980  64.360  1.00 44.87      A
ATOM    440  CD1 ILE A  63      21.498   7.760  65.172  1.00 49.37      A
ATOM    441  C   ILE A  63      20.486  11.641  63.251  1.00 43.47      A
ATOM    442  O   ILE A  63      19.539  11.763  62.472  1.00 44.55      A
ATOM    443  N   ASP A  64      21.497  12.505  63.309  1.00 41.40      A
ATOM    444  CA  ASP A  64      21.556  13.682  62.454  1.00 39.74      A
ATOM    445  CB  ASP A  64      22.295  14.827  63.152  1.00 44.20      A
ATOM    446  CG  ASP A  64      21.477  15.483  64.237  1.00 45.89      A
ATOM    447  OD1 ASP A  64      20.431  16.094  63.921  1.00 49.96      A
ATOM    448  OD2 ASP A  64      21.887  15.397  65.411  1.00 49.43      A
ATOM    449  C   ASP A  64      22.250  13.447  61.133  1.00 40.83      A
ATOM    450  O   ASP A  64      23.431  13.107  61.100  1.00 41.64      A
ATOM    451  N   VAL A  65      21.518  13.637  60.044  1.00 37.89      A
ATOM    452  CA  VAL A  65      22.088  13.513  58.716  1.00 37.35      A
ATOM    453  CB  VAL A  65      21.153  12.743  57.755  1.00 32.89      A
ATOM    454  CG1 VAL A  65      21.801  12.617  56.396  1.00 34.14      A
ATOM    455  CG2 VAL A  65      20.846  11.363  58.310  1.00 32.51      A
ATOM    456  C   VAL A  65      22.195  14.976  58.274  1.00 40.86      A
ATOM    457  O   VAL A  65      21.253  15.536  57.715  1.00 40.12      A
ATOM    458  N   LYS A  66      23.326  15.611  58.572  1.00 43.11      A
ATOM    459  CA  LYS A  66      23.512  17.004  58.195  1.00 44.83      A
ATOM    460  CB  LYS A  66      23.264  17.928  59.391  1.00 46.81      A
ATOM    461  CG  LYS A  66      24.279  17.808  60.517  1.00 54.55      A
ATOM    462  CD  LYS A  66      24.200  19.040  61.417  1.00 59.11      A
ATOM    463  CE  LYS A  66      25.362  19.109  62.400  1.00 65.08      A
ATOM    464  NZ  LYS A  66      25.465  20.481  63.022  1.00 68.64      A
ATOM    465  C   LYS A  66      24.887  17.299  57.613  1.00 45.03      A
ATOM    466  O   LYS A  66      25.886  16.658  57.959  1.00 42.46      A
ATOM    467  N   ASP A  67      24.922  18.289  56.730  1.00 41.84      A
ATOM    468  CA  ASP A  67      26.153  18.705  56.073  1.00 45.14      A
ATOM    469  CB  ASP A  67      27.120  19.337  57.081  1.00 44.43      A
ATOM    470  CG  ASP A  67      26.547  20.571  57.738  1.00 43.57      A
ATOM    471  OD1 ASP A  67      26.134  21.502  57.010  1.00 46.44      A
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ATOM	472	OD2	ASP	A	67	26.506	20.611	58.985	1.00	49.07	A
ATOM	473	C	ASP	A	67	26.833	17.543	55.364	1.00	43.94	A
ATOM	474	O	ASP	A	67	28.055	17.394	55.430	1.00	43.52	A
ATOM	475	N	VAL	A	68	26.029	16.717	54.698	1.00	42.22	A
ATOM	476	CA	VAL	A	68	26.540	15.581	53.940	1.00	39.27	A
ATOM	477	CB	VAL	A	68	26.442	14.267	54.732	1.00	40.27	A
ATOM	478	CG1	VAL	A	68	27.410	14.303	55.912	1.00	41.48	A
ATOM	479	CG2	VAL	A	68	25.019	14.052	55.213	1.00	36.36	A
ATOM	480	C	VAL	A	68	25.734	15.456	52.656	1.00	40.72	A
ATOM	481	O	VAL	A	68	24.628	15.993	52.553	1.00	38.86	A
ATOM	482	N	SER	A	69	26.297	14.757	51.679	1.00	37.90	A
ATOM	483	CA	SER	A	69	25.639	14.572	50.397	1.00	36.49	A
ATOM	484	CB	SER	A	69	26.115	15.621	49.388	1.00	36.51	A
ATOM	485	OG	SER	A	69	25.610	16.906	49.699	1.00	42.04	A
ATOM	486	C	SER	A	69	25.935	13.200	49.836	1.00	37.37	A
ATOM	487	O	SER	A	69	26.969	12.611	50.135	1.00	38.57	A
ATOM	488	N	ASN	A	70	25.011	12.701	49.022	1.00	33.82	A
ATOM	489	CA	ASN	A	70	25.176	11.410	48.384	1.00	35.12	A
ATOM	490	CB	ASN	A	70	26.382	11.489	47.448	1.00	33.76	A
ATOM	491	CG	ASN	A	70	26.435	12.818	46.703	1.00	38.78	A
ATOM	492	OD1	ASN	A	70	25.481	13.199	46.019	1.00	37.16	A
ATOM	493	ND2	ASN	A	70	27.545	13.540	46.846	1.00	38.07	A
ATOM	494	C	ASN	A	70	25.352	10.330	49.431	1.00	34.03	A
ATOM	495	O	ASN	A	70	26.414	9.722	49.538	1.00	34.34	A
ATOM	496	N	VAL	A	71	24.298	10.112	50.212	1.00	34.47	A
ATOM	497	CA	VAL	A	71	24.299	9.108	51.265	1.00	32.89	A
ATOM	498	CB	VAL	A	71	24.348	9.778	52.663	1.00	32.35	A
ATOM	499	CG1	VAL	A	71	24.300	8.722	53.749	1.00	34.06	A
ATOM	500	CG2	VAL	A	71	25.623	10.612	52.806	1.00	37.91	A
ATOM	501	C	VAL	A	71	23.047	8.226	51.206	1.00	33.60	A
ATOM	502	O	VAL	A	71	21.964	8.708	50.887	1.00	32.30	A
ATOM	503	N	SER	A	72	23.217	6.934	51.493	1.00	30.03	A
ATOM	504	CA	SER	A	72	22.114	5.973	51.548	1.00	31.46	A
ATOM	505	CB	SER	A	72	22.223	4.910	50.444	1.00	32.79	A
ATOM	506	OG	SER	A	72	21.869	5.430	49.174	1.00	32.49	A
ATOM	507	C	SER	A	72	22.183	5.271	52.904	1.00	35.34	A
ATOM	508	O	SER	A	72	23.235	4.765	53.292	1.00	38.11	A
ATOM	509	N	ILE	A	73	21.072	5.269	53.633	1.00	34.37	A
ATOM	510	CA	ILE	A	73	20.999	4.601	54.918	1.00	32.19	A
ATOM	511	CB	ILE	A	73	20.591	5.565	56.050	1.00	34.48	A
ATOM	512	CG2	ILE	A	73	20.431	4.788	57.354	1.00	31.99	A
ATOM	513	CG1	ILE	A	73	21.654	6.651	56.211	1.00	32.17	A
ATOM	514	CD1	ILE	A	73	21.365	7.645	57.318	1.00	36.97	A
ATOM	515	C	ILE	A	73	19.916	3.569	54.710	1.00	33.15	A
ATOM	516	O	ILE	A	73	18.736	3.908	54.648	1.00	32.77	A
ATOM	517	N	VAL	A	74	20.324	2.311	54.585	1.00	34.34	A
ATOM	518	CA	VAL	A	74	19.386	1.225	54.327	1.00	33.77	A
ATOM	519	CB	VAL	A	74	19.586	.677	52.895	1.00	35.75	A
ATOM	520	CG1	VAL	A	74	19.415	1.791	51.886	1.00	32.70	A
ATOM	521	CG2	VAL	A	74	20.976	.084	52.753	1.00	38.37	A
ATOM	522	C	VAL	A	74	19.493	.056	55.293	1.00	35.02	A
ATOM	523	O	VAL	A	74	20.582	-.307	55.726	1.00	37.30	A
ATOM	524	N	GLY	A	75	18.355	-.544	55.615	1.00	33.91	A
ATOM	525	CA	GLY	A	75	18.367	-1.682	56.509	1.00	35.02	A
ATOM	526	C	GLY	A	75	18.687	-2.940	55.727	1.00	38.83	A
ATOM	527	O	GLY	A	75	18.385	-3.032	54.536	1.00	38.11	A
ATOM	528	N	SER	A	76	19.314	-3.908	56.389	1.00	42.80	A
ATOM	529	CA	SER	A	76	19.665	-5.170	55.751	1.00	42.73	A
ATOM	530	CB	SER	A	76	21.051	-5.618	56.212	1.00	44.32	A
ATOM	531	OG	SER	A	76	21.488	-6.749	55.477	1.00	53.38	A
ATOM	532	C	SER	A	76	18.613	-6.206	56.142	1.00	41.79	A
ATOM	533	O	SER	A	76	18.341	-6.411	57.324	1.00	45.37	A
ATOM	534	N	GLY	A	77	18.014	-6.856	55.151	1.00	41.32	A
ATOM	535	CA	GLY	A	77	16.994	-7.845	55.452	1.00	40.12	A
ATOM	536	C	GLY	A	77	15.861	-7.181	56.203	1.00	42.47	A
ATOM	537	O	GLY	A	77	15.323	-6.160	55.755	1.00	43.53	A
ATOM	538	N	THR	A	78	15.495	-7.747	57.348	1.00	41.81	A
ATOM	539	CA	THR	A	78	14.429	-7.183	58.159	1.00	40.95	A
ATOM	540	CB	THR	A	78	13.266	-8.174	58.355	1.00	42.61	A

ATOM	541	OG1	THR	A	78	13.733	-9.326	59.066	1.00	44.55	A
ATOM	542	CG2	THR	A	78	12.707	-8.617	57.016	1.00	43.39	A
ATOM	543	C	THR	A	78	14.977	-6.817	59.524	1.00	41.40	A
ATOM	544	O	THR	A	78	14.225	-6.758	60.491	1.00	44.91	A
ATOM	545	N	LYS	A	79	16.280	-6.555	59.601	1.00	45.59	A
ATOM	546	CA	LYS	A	79	16.927	-6.209	60.877	1.00	47.57	A
ATOM	547	CB	LYS	A	79	18.230	-7.006	61.041	1.00	50.86	A
ATOM	548	CG	LYS	A	79	18.159	-8.442	60.512	1.00	56.96	A
ATOM	549	CD	LYS	A	79	19.494	-9.177	60.713	1.00	64.27	A
ATOM	550	CE	LYS	A	79	19.575	-10.447	59.853	1.00	70.93	A
ATOM	551	NZ	LYS	A	79	18.438	-11.401	60.089	1.00	75.08	A
ATOM	552	C	LYS	A	79	17.241	-4.718	61.003	1.00	45.94	A
ATOM	553	O	LYS	A	79	17.738	-4.259	62.032	1.00	46.91	A
ATOM	554	N	GLY	A	80	16.970	-3.953	59.957	1.00	43.23	A
ATOM	555	CA	GLY	A	80	17.239	-2.532	60.047	1.00	40.72	A
ATOM	556	C	GLY	A	80	16.178	-1.875	60.908	1.00	41.12	A
ATOM	557	O	GLY	A	80	15.098	-1.537	60.417	1.00	41.75	A
ATOM	558	N	GLU	A	81	16.467	-1.688	62.192	1.00	40.03	A
ATOM	559	CA	GLU	A	81	15.481	-1.082	63.083	1.00	41.30	A
ATOM	560	CB	GLU	A	81	14.812	-2.169	63.924	1.00	40.04	A
ATOM	561	CG	GLU	A	81	13.887	-1.638	64.999	1.00	42.03	A
ATOM	562	CD	GLU	A	81	13.296	-2.746	65.842	1.00	42.58	A
ATOM	563	OE1	GLU	A	81	13.979	-3.780	66.004	1.00	48.88	A
ATOM	564	OE2	GLU	A	81	12.162	-2.580	66.350	1.00	44.10	A
ATOM	565	C	GLU	A	81	15.977	.026	64.008	1.00	41.69	A
ATOM	566	O	GLU	A	81	17.052	-.072	64.605	1.00	43.83	A
ATOM	567	N	LEU	A	82	15.173	1.083	64.109	1.00	39.76	A
ATOM	568	CA	LEU	A	82	15.460	2.216	64.981	1.00	39.11	A
ATOM	569	CB	LEU	A	82	15.527	3.524	64.193	1.00	32.46	A
ATOM	570	CG	LEU	A	82	16.863	3.838	63.524	1.00	36.24	A
ATOM	571	CD1	LEU	A	82	17.125	2.837	62.424	1.00	37.09	A
ATOM	572	CD2	LEU	A	82	16.841	5.261	62.971	1.00	38.34	A
ATOM	573	C	LEU	A	82	14.307	2.263	65.962	1.00	40.97	A
ATOM	574	O	LEU	A	82	13.183	2.611	65.593	1.00	42.80	A
ATOM	575	N	LYS	A	83	14.591	1.898	67.213	1.00	44.78	A
ATOM	576	CA	LYS	A	83	13.578	1.855	68.257	1.00	42.33	A
ATOM	577	CB	LYS	A	83	13.618	.479	68.938	1.00	44.61	A
ATOM	578	CG	LYS	A	83	12.623	.280	70.065	1.00	47.05	A
ATOM	579	CD	LYS	A	83	12.670	-1.168	70.553	1.00	54.95	A
ATOM	580	CE	LYS	A	83	11.769	-1.387	71.771	1.00	58.19	A
ATOM	581	NZ	LYS	A	83	11.656	-2.844	72.124	1.00	63.24	A
ATOM	582	C	LYS	A	83	13.776	2.967	69.280	1.00	43.37	A
ATOM	583	O	LYS	A	83	14.785	3.006	69.993	1.00	43.07	A
ATOM	584	N	GLY	A	84	12.805	3.877	69.337	1.00	41.50	A
ATOM	585	CA	GLY	A	84	12.864	4.983	70.274	1.00	38.43	A
ATOM	586	C	GLY	A	84	13.787	6.085	69.819	1.00	40.91	A
ATOM	587	O	GLY	A	84	13.920	7.118	70.483	1.00	42.36	A
ATOM	588	N	ILE	A	85	14.422	5.868	68.675	1.00	38.96	A
ATOM	589	CA	ILE	A	85	15.346	6.842	68.119	1.00	40.25	A
ATOM	590	CB	ILE	A	85	16.768	6.255	68.102	1.00	39.50	A
ATOM	591	CG2	ILE	A	85	16.759	4.901	67.421	1.00	44.37	A
ATOM	592	CG1	ILE	A	85	17.733	7.241	67.457	1.00	38.98	A
ATOM	593	CD1	ILE	A	85	18.015	8.437	68.338	1.00	47.32	A
ATOM	594	C	ILE	A	85	14.912	7.227	66.697	1.00	41.93	A
ATOM	595	O	ILE	A	85	14.503	6.359	65.917	1.00	40.01	A
ATOM	596	N	GLY	A	86	14.998	8.521	66.370	1.00	39.30	A
ATOM	597	CA	GLY	A	86	14.600	8.991	65.051	1.00	38.51	A
ATOM	598	C	GLY	A	86	15.717	9.562	64.189	1.00	40.84	A
ATOM	599	O	GLY	A	86	16.869	9.681	64.624	1.00	37.96	A
ATOM	600	N	ILE	A	87	15.366	9.920	62.955	1.00	37.67	A
ATOM	601	CA	ILE	A	87	16.318	10.486	62.003	1.00	32.62	A
ATOM	602	CB	ILE	A	87	16.382	9.633	60.714	1.00	33.06	A
ATOM	603	CG2	ILE	A	87	17.235	10.328	59.653	1.00	30.95	A
ATOM	604	CG1	ILE	A	87	16.940	8.247	61.043	1.00	38.70	A
ATOM	605	CD1	ILE	A	87	16.958	7.280	59.857	1.00	38.07	A
ATOM	606	C	ILE	A	87	15.914	11.903	61.623	1.00	29.64	A
ATOM	607	O	ILE	A	87	14.737	12.189	61.414	1.00	33.55	A
ATOM	608	N	LYS	A	88	16.894	12.792	61.541	1.00	30.92	A
ATOM	609	CA	LYS	A	88	16.631	14.173	61.156	1.00	31.16	A

ATOM	610	CB	LYS	A	88	16.841	15.118	62.336	1.00	35.55	A
ATOM	611	CG	LYS	A	88	16.625	16.584	61.975	1.00	37.46	A
ATOM	612	CD	LYS	A	88	17.062	17.505	63.097	1.00	43.37	A
ATOM	613	CE	LYS	A	88	16.932	18.973	62.693	1.00	49.25	A
ATOM	614	NZ	LYS	A	88	15.523	19.333	62.304	1.00	52.39	A
ATOM	615	C	LYS	A	88	17.592	14.535	60.035	1.00	33.33	A
ATOM	616	O	LYS	A	88	18.809	14.487	60.217	1.00	36.09	A
ATOM	617	N	ILE	A	89	17.039	14.873	58.873	1.00	32.19	A
ATOM	618	CA	ILE	A	89	17.827	15.245	57.697	1.00	33.32	A
ATOM	619	CB	ILE	A	89	17.237	14.608	56.425	1.00	31.57	A
ATOM	620	CG2	ILE	A	89	18.017	15.042	55.200	1.00	37.70	A
ATOM	621	CG1	ILE	A	89	17.266	13.091	56.561	1.00	36.06	A
ATOM	622	CD1	ILE	A	89	16.572	12.365	55.432	1.00	37.21	A
ATOM	623	C	ILE	A	89	17.782	16.767	57.586	1.00	35.59	A
ATOM	624	O	ILE	A	89	16.709	17.362	57.524	1.00	35.86	A
ATOM	625	N	TRP	A	90	18.954	17.387	57.546	1.00	36.73	A
ATOM	626	CA	TRP	A	90	19.047	18.842	57.508	1.00	37.11	A
ATOM	627	CB	TRP	A	90	18.963	19.327	58.963	1.00	42.84	A
ATOM	628	CG	TRP	A	90	19.147	20.790	59.199	1.00	49.35	A
ATOM	629	CD2	TRP	A	90	19.864	21.388	60.284	1.00	52.87	A
ATOM	630	CE2	TRP	A	90	19.726	22.789	60.155	1.00	54.66	A
ATOM	631	CE3	TRP	A	90	20.609	20.875	61.357	1.00	57.65	A
ATOM	632	CD1	TRP	A	90	18.618	21.820	58.472	1.00	50.83	A
ATOM	633	NE1	TRP	A	90	18.963	23.027	59.041	1.00	53.40	A
ATOM	634	CZ2	TRP	A	90	20.307	23.687	61.060	1.00	57.24	A
ATOM	635	CZ3	TRP	A	90	21.188	21.769	62.259	1.00	58.23	A
ATOM	636	CH2	TRP	A	90	21.033	23.159	62.102	1.00	57.53	A
ATOM	637	C	TRP	A	90	20.345	19.300	56.818	1.00	35.72	A
ATOM	638	O	TRP	A	90	21.417	18.769	57.094	1.00	38.20	A
ATOM	639	N	ARG	A	91	20.248	20.280	55.922	1.00	36.52	A
ATOM	640	CA	ARG	A	91	21.420	20.763	55.188	1.00	41.04	A
ATOM	641	CB	ARG	A	91	22.397	21.467	56.146	1.00	41.60	A
ATOM	642	CG	ARG	A	91	21.848	22.759	56.756	1.00	42.35	A
ATOM	643	CD	ARG	A	91	22.437	23.034	58.139	1.00	50.28	A
ATOM	644	NE	ARG	A	91	23.829	23.487	58.109	1.00	50.50	A
ATOM	645	CZ	ARG	A	91	24.214	24.690	57.683	1.00	55.10	A
ATOM	646	NH1	ARG	A	91	25.501	25.034	57.692	1.00	55.97	A
ATOM	647	NH2	ARG	A	91	23.311	25.555	57.243	1.00	59.56	A
ATOM	648	C	ARG	A	91	22.110	19.573	54.510	1.00	41.57	A
ATOM	649	O	ARG	A	91	23.326	19.406	54.618	1.00	43.00	A
ATOM	650	N	ALA	A	92	21.321	18.751	53.815	1.00	41.55	A
ATOM	651	CA	ALA	A	92	21.827	17.557	53.130	1.00	37.52	A
ATOM	652	CB	ALA	A	92	21.568	16.318	53.995	1.00	32.47	A
ATOM	653	C	ALA	A	92	21.152	17.392	51.775	1.00	35.66	A
ATOM	654	O	ALA	A	92	19.996	17.764	51.615	1.00	38.99	A
ATOM	655	N	ASN	A	93	21.866	16.832	50.802	1.00	35.21	A
ATOM	656	CA	ASN	A	93	21.300	16.632	49.467	1.00	35.47	A
ATOM	657	CB	ASN	A	93	21.890	17.633	48.470	1.00	40.52	A
ATOM	658	CG	ASN	A	93	21.680	19.070	48.897	1.00	51.09	A
ATOM	659	OD1	ASN	A	93	20.546	19.498	49.160	1.00	53.38	A
ATOM	660	ND2	ASN	A	93	22.772	19.830	48.977	1.00	54.12	A
ATOM	661	C	ASN	A	93	21.561	15.227	48.959	1.00	35.48	A
ATOM	662	O	ASN	A	93	22.562	14.610	49.317	1.00	32.99	A
ATOM	663	N	ASN	A	94	20.661	14.742	48.104	1.00	34.93	A
ATOM	664	CA	ASN	A	94	20.769	13.415	47.514	1.00	31.08	A
ATOM	665	CB	ASN	A	94	21.941	13.380	46.533	1.00	32.67	A
ATOM	666	CG	ASN	A	94	22.013	12.081	45.758	1.00	34.77	A
ATOM	667	OD1	ASN	A	94	20.990	11.453	45.485	1.00	33.72	A
ATOM	668	ND2	ASN	A	94	23.224	11.679	45.382	1.00	36.43	A
ATOM	669	C	ASN	A	94	20.942	12.370	48.602	1.00	31.96	A
ATOM	670	O	ASN	A	94	22.008	11.776	48.755	1.00	32.62	A
ATOM	671	N	ILE	A	95	19.866	12.158	49.355	1.00	32.79	A
ATOM	672	CA	ILE	A	95	19.836	11.209	50.456	1.00	29.64	A
ATOM	673	CB	ILE	A	95	19.558	11.936	51.799	1.00	29.86	A
ATOM	674	CG2	ILE	A	95	19.649	10.954	52.952	1.00	28.03	A
ATOM	675	CG1	ILE	A	95	20.566	13.073	52.009	1.00	31.41	A
ATOM	676	CD1	ILE	A	95	22.007	12.614	52.084	1.00	26.75	A
ATOM	677	C	ILE	A	95	18.744	10.153	50.249	1.00	33.04	A
ATOM	678	O	ILE	A	95	17.635	10.470	49.806	1.00	28.56	A

ATOM	679	N	ILE	A	96	19.065	8.904	50.585	1.00	30.40	A
ATOM	680	CA	ILE	A	96	18.121	7.805	50.446	1.00	27.12	A
ATOM	681	CB	ILE	A	96	18.584	6.799	49.361	1.00	25.27	A
ATOM	682	CG2	ILE	A	96	17.722	5.543	49.411	1.00	29.82	A
ATOM	683	CG1	ILE	A	96	18.522	7.450	47.975	1.00	22.62	A
ATOM	684	CD1	ILE	A	96	18.861	6.493	46.827	1.00	24.48	A
ATOM	685	C	ILE	A	96	17.959	7.060	51.764	1.00	24.17	A
ATOM	686	O	ILE	A	96	18.938	6.639	52.371	1.00	29.32	A
ATOM	687	N	ILE	A	97	16.717	6.925	52.209	1.00	29.14	A
ATOM	688	CA	ILE	A	97	16.387	6.206	53.439	1.00	27.30	A
ATOM	689	CB	ILE	A	97	15.607	7.102	54.426	1.00	25.57	A
ATOM	690	CG2	ILE	A	97	15.408	6.371	55.739	1.00	26.30	A
ATOM	691	CG1	ILE	A	97	16.358	8.411	54.663	1.00	27.73	A
ATOM	692	CD1	ILE	A	97	17.688	8.250	55.370	1.00	33.92	A
ATOM	693	C	ILE	A	97	15.478	5.053	52.988	1.00	28.25	A
ATOM	694	O	ILE	A	97	14.331	5.286	52.609	1.00	20.04	A
ATOM	695	N	ARG	A	98	15.989	3.821	53.008	1.00	30.58	A
ATOM	696	CA	ARG	A	98	15.213	2.659	52.560	1.00	31.47	A
ATOM	697	CB	ARG	A	98	15.666	2.180	51.181	1.00	33.93	A
ATOM	698	CG	ARG	A	98	15.367	3.050	49.998	1.00	37.69	A
ATOM	699	CD	ARG	A	98	15.820	2.323	48.722	1.00	33.96	A
ATOM	700	NE	ARG	A	98	14.717	1.725	47.969	1.00	35.28	A
ATOM	701	CZ	ARG	A	98	14.876	.995	46.866	1.00	32.42	A
ATOM	702	NH1	ARG	A	98	13.827	.494	46.228	1.00	28.84	A
ATOM	703	NH2	ARG	A	98	16.094	.751	46.405	1.00	35.66	A
ATOM	704	C	ARG	A	98	15.288	1.427	53.432	1.00	34.16	A
ATOM	705	O	ARG	A	98	16.335	1.104	53.984	1.00	36.25	A
ATOM	706	N	ASN	A	99	14.173	.716	53.507	1.00	30.39	A
ATOM	707	CA	ASN	A	99	14.096	-.538	54.239	1.00	32.90	A
ATOM	708	CB	ASN	A	99	14.998	-1.566	53.544	1.00	27.39	A
ATOM	709	CG	ASN	A	99	14.611	-2.990	53.870	1.00	33.45	A
ATOM	710	OD1	ASN	A	99	13.430	-3.338	53.858	1.00	29.67	A
ATOM	711	ND2	ASN	A	99	15.605	-3.828	54.158	1.00	35.17	A
ATOM	712	C	ASN	A	99	14.418	-.477	55.730	1.00	33.58	A
ATOM	713	O	ASN	A	99	15.160	-1.308	56.246	1.00	35.29	A
ATOM	714	N	LEU	A	100	13.845	.498	56.424	1.00	35.67	A
ATOM	715	CA	LEU	A	100	14.065	.639	57.858	1.00	33.56	A
ATOM	716	CB	LEU	A	100	14.809	1.936	58.172	1.00	33.16	A
ATOM	717	CG	LEU	A	100	16.268	2.066	57.743	1.00	34.93	A
ATOM	718	CD1	LEU	A	100	16.730	3.493	58.003	1.00	34.78	A
ATOM	719	CD2	LEU	A	100	17.126	1.060	58.501	1.00	30.92	A
ATOM	720	C	LEU	A	100	12.758	.649	58.621	1.00	34.42	A
ATOM	721	O	LEU	A	100	11.726	1.068	58.105	1.00	32.49	A
ATOM	722	N	LYS	A	101	12.807	.178	59.858	1.00	34.84	A
ATOM	723	CA	LYS	A	101	11.634	.179	60.712	1.00	35.09	A
ATOM	724	CB	LYS	A	101	11.384	-1.213	61.302	1.00	36.72	A
ATOM	725	CG	LYS	A	101	10.168	-1.266	62.214	1.00	40.09	A
ATOM	726	CD	LYS	A	101	9.985	-2.633	62.880	1.00	44.09	A
ATOM	727	CE	LYS	A	101	9.606	-3.708	61.869	1.00	46.68	A
ATOM	728	NZ	LYS	A	101	9.145	-4.954	62.559	1.00	48.42	A
ATOM	729	C	LYS	A	101	11.970	1.172	61.820	1.00	37.33	A
ATOM	730	O	LYS	A	101	12.835	.912	62.651	1.00	39.76	A
ATOM	731	N	ILE	A	102	11.309	2.324	61.811	1.00	34.07	A
ATOM	732	CA	ILE	A	102	11.558	3.355	62.810	1.00	30.98	A
ATOM	733	CB	ILE	A	102	11.961	4.664	62.130	1.00	31.41	A
ATOM	734	CG2	ILE	A	102	12.411	5.683	63.171	1.00	32.47	A
ATOM	735	CG1	ILE	A	102	13.079	4.383	61.125	1.00	32.05	A
ATOM	736	CD1	ILE	A	102	13.475	5.577	60.271	1.00	29.24	A
ATOM	737	C	ILE	A	102	10.261	3.543	63.573	1.00	34.14	A
ATOM	738	O	ILE	A	102	9.219	3.773	62.966	1.00	32.61	A
ATOM	739	N	HIS	A	103	10.317	3.454	64.903	1.00	33.67	A
ATOM	740	CA	HIS	A	103	9.089	3.564	65.690	1.00	36.37	A
ATOM	741	CB	HIS	A	103	8.385	2.204	65.687	1.00	37.60	A
ATOM	742	CG	HIS	A	103	9.230	1.090	66.228	1.00	39.32	A
ATOM	743	CD2	HIS	A	103	10.313	.462	65.711	1.00	39.93	A
ATOM	744	ND1	HIS	A	103	9.018	.525	67.467	1.00	40.16	A
ATOM	745	CE1	HIS	A	103	9.932	-.401	67.691	1.00	36.52	A
ATOM	746	NE2	HIS	A	103	10.730	-.460	66.641	1.00	39.48	A
ATOM	747	C	HIS	A	103	9.188	4.049	67.139	1.00	37.45	A

ATOM	748	O	HIS	A	103	10.228	3.937	67.793	1.00	35.61	A
ATOM	749	N	GLU	A	104	8.069	4.589	67.619	1.00	38.77	A
ATOM	750	CA	GLU	A	104	7.918	5.072	68.987	1.00	36.76	A
ATOM	751	CB	GLU	A	104	7.667	3.860	69.891	1.00	39.15	A
ATOM	752	CG	GLU	A	104	6.564	2.959	69.321	1.00	39.74	A
ATOM	753	CD	GLU	A	104	6.514	1.567	69.937	1.00	42.91	A
ATOM	754	OE1	GLU	A	104	5.755	1.368	70.910	1.00	46.24	A
ATOM	755	OE2	GLU	A	104	7.234	.667	69.448	1.00	41.88	A
ATOM	756	C	GLU	A	104	9.092	5.908	69.487	1.00	38.67	A
ATOM	757	O	GLU	A	104	9.816	5.513	70.407	1.00	38.16	A
ATOM	758	N	VAL	A	105	9.256	7.082	68.882	1.00	35.94	A
ATOM	759	CA	VAL	A	105	10.337	8.000	69.220	1.00	36.78	A
ATOM	760	CB	VAL	A	105	10.858	8.691	67.942	1.00	34.11	A
ATOM	761	CG1	VAL	A	105	12.085	9.522	68.252	1.00	30.07	A
ATOM	762	CG2	VAL	A	105	11.157	7.642	66.880	1.00	29.88	A
ATOM	763	C	VAL	A	105	9.874	9.073	70.212	1.00	41.87	A
ATOM	764	O	VAL	A	105	9.239	10.060	69.821	1.00	40.97	A
ATOM	765	N	ALA	A	106	10.191	8.885	71.493	1.00	43.01	A
ATOM	766	CA	ALA	A	106	9.785	9.847	72.517	1.00	45.12	A
ATOM	767	CB	ALA	A	106	9.329	9.125	73.768	1.00	45.28	A
ATOM	768	C	ALA	A	106	10.909	10.806	72.864	1.00	47.40	A
ATOM	769	O	ALA	A	106	10.739	11.691	73.708	1.00	48.23	A
ATOM	770	N	SER	A	107	12.049	10.641	72.200	1.00	48.12	A
ATOM	771	CA	SER	A	107	13.209	11.485	72.453	1.00	48.04	A
ATOM	772	CB	SER	A	107	14.441	10.605	72.675	1.00	48.44	A
ATOM	773	OG	SER	A	107	14.482	9.565	71.709	1.00	52.60	A
ATOM	774	C	SER	A	107	13.468	12.453	71.312	1.00	49.25	A
ATOM	775	O	SER	A	107	12.806	12.396	70.262	1.00	49.32	A
ATOM	776	N	GLY	A	108	14.437	13.342	71.519	1.00	46.97	A
ATOM	777	CA	GLY	A	108	14.775	14.318	70.500	1.00	47.45	A
ATOM	778	C	GLY	A	108	13.556	15.080	70.019	1.00	46.66	A
ATOM	779	O	GLY	A	108	12.761	15.563	70.828	1.00	45.65	A
ATOM	780	N	ASP	A	109	13.403	15.179	68.699	1.00	45.77	A
ATOM	781	CA	ASP	A	109	12.279	15.891	68.096	1.00	41.98	A
ATOM	782	CB	ASP	A	109	12.601	16.229	66.635	1.00	46.32	A
ATOM	783	CG	ASP	A	109	13.732	17.230	66.505	1.00	51.94	A
ATOM	784	OD1	ASP	A	109	14.182	17.497	65.364	1.00	55.23	A
ATOM	785	OD2	ASP	A	109	14.171	17.763	67.547	1.00	57.30	A
ATOM	786	C	ASP	A	109	10.988	15.083	68.168	1.00	39.10	A
ATOM	787	O	ASP	A	109	9.917	15.579	67.811	1.00	40.64	A
ATOM	788	N	LYS	A	110	11.097	13.841	68.630	1.00	35.20	A
ATOM	789	CA	LYS	A	110	9.944	12.949	68.759	1.00	40.15	A
ATOM	790	CB	LYS	A	110	8.908	13.582	69.705	1.00	42.88	A
ATOM	791	CG	LYS	A	110	9.478	13.924	71.096	1.00	45.24	A
ATOM	792	CD	LYS	A	110	8.532	14.812	71.898	1.00	51.78	A
ATOM	793	CE	LYS	A	110	7.448	14.028	72.617	1.00	51.74	A
ATOM	794	NZ	LYS	A	110	7.941	13.451	73.914	1.00	55.06	A
ATOM	795	C	LYS	A	110	9.298	12.596	67.405	1.00	39.62	A
ATOM	796	O	LYS	A	110	8.102	12.289	67.331	1.00	41.05	A
ATOM	797	N	ASP	A	111	10.100	12.631	66.341	1.00	38.75	A
ATOM	798	CA	ASP	A	111	9.630	12.304	64.992	1.00	36.88	A
ATOM	799	CB	ASP	A	111	9.896	13.472	64.030	1.00	35.33	A
ATOM	800	CG	ASP	A	111	9.279	14.774	64.495	1.00	33.91	A
ATOM	801	OD1	ASP	A	111	9.881	15.839	64.221	1.00	34.48	A
ATOM	802	OD2	ASP	A	111	8.190	14.736	65.111	1.00	35.61	A
ATOM	803	C	ASP	A	111	10.402	11.085	64.482	1.00	34.31	A
ATOM	804	O	ASP	A	111	11.598	10.948	64.746	1.00	36.09	A
ATOM	805	N	ALA	A	112	9.730	10.200	63.758	1.00	32.63	A
ATOM	806	CA	ALA	A	112	10.407	9.033	63.208	1.00	28.90	A
ATOM	807	CB	ALA	A	112	9.410	8.128	62.502	1.00	30.88	A
ATOM	808	C	ALA	A	112	11.433	9.555	62.210	1.00	32.07	A
ATOM	809	O	ALA	A	112	12.614	9.209	62.268	1.00	32.71	A
ATOM	810	N	ILE	A	113	10.962	10.387	61.283	1.00	31.13	A
ATOM	811	CA	ILE	A	113	11.824	10.994	60.280	1.00	28.78	A
ATOM	812	CB	ILE	A	113	11.665	10.348	58.891	1.00	32.20	A
ATOM	813	CG2	ILE	A	113	12.565	11.068	57.883	1.00	31.31	A
ATOM	814	CG1	ILE	A	113	12.051	8.874	58.943	1.00	32.74	A
ATOM	815	CD1	ILE	A	113	11.908	8.176	57.609	1.00	35.19	A
ATOM	816	C	ILE	A	113	11.450	12.455	60.141	1.00	27.97	A

ATOM	817	O	ILE	A	113	10.274	12.793	59.965	1.00	30.03	A
ATOM	818	N	GLY	A	114	12.449	13.324	60.226	1.00	29.47	A
ATOM	819	CA	GLY	A	114	12.200	14.744	60.086	1.00	26.85	A
ATOM	820	C	GLY	A	114	13.151	15.356	59.075	1.00	29.61	A
ATOM	821	O	GLY	A	114	14.352	15.098	59.106	1.00	31.07	A
ATOM	822	N	ILE	A	115	12.615	16.146	58.156	1.00	28.59	A
ATOM	823	CA	ILE	A	115	13.439	16.809	57.161	1.00	28.70	A
ATOM	824	CB	ILE	A	115	13.021	16.435	55.728	1.00	27.59	A
ATOM	825	CG2	ILE	A	115	13.874	17.196	54.734	1.00	27.93	A
ATOM	826	CG1	ILE	A	115	13.176	14.926	55.510	1.00	29.30	A
ATOM	827	CD1	ILE	A	115	12.762	14.473	54.127	1.00	33.21	A
ATOM	828	C	ILE	A	115	13.306	18.323	57.325	1.00	31.73	A
ATOM	829	O	ILE	A	115	12.194	18.859	57.385	1.00	29.11	A
ATOM	830	N	GLU	A	116	14.441	19.009	57.397	1.00	31.89	A
ATOM	831	CA	GLU	A	116	14.431	20.460	57.543	1.00	34.65	A
ATOM	832	CB	GLU	A	116	14.993	20.854	58.905	1.00	36.37	A
ATOM	833	CG	GLU	A	116	14.511	22.212	59.381	1.00	46.04	A
ATOM	834	CD	GLU	A	116	15.187	22.660	60.663	1.00	46.34	A
ATOM	835	OE1	GLU	A	116	15.326	21.835	61.595	1.00	43.32	A
ATOM	836	OE2	GLU	A	116	15.567	23.846	60.728	1.00	48.80	A
ATOM	837	C	GLU	A	116	15.271	21.088	56.444	1.00	33.52	A
ATOM	838	O	GLU	A	116	16.373	20.618	56.156	1.00	34.32	A
ATOM	839	N	GLY	A	117	14.748	22.139	55.821	1.00	30.79	A
ATOM	840	CA	GLY	A	117	15.489	22.803	54.767	1.00	33.26	A
ATOM	841	C	GLY	A	117	16.684	23.545	55.342	1.00	35.78	A
ATOM	842	O	GLY	A	117	16.709	23.827	56.535	1.00	33.16	A
ATOM	843	N	PRO	A	118	17.696	23.861	54.520	1.00	36.52	A
ATOM	844	CD	PRO	A	118	18.883	24.662	54.877	1.00	38.12	A
ATOM	845	CA	PRO	A	118	17.704	23.521	53.097	1.00	36.75	A
ATOM	846	CB	PRO	A	118	18.691	24.527	52.516	1.00	38.38	A
ATOM	847	CG	PRO	A	118	19.716	24.617	53.607	1.00	39.57	A
ATOM	848	C	PRO	A	118	18.143	22.074	52.877	1.00	36.69	A
ATOM	849	O	PRO	A	118	19.175	21.642	53.394	1.00	38.13	A
ATOM	850	N	SER	A	119	17.339	21.333	52.119	1.00	33.97	A
ATOM	851	CA	SER	A	119	17.604	19.935	51.798	1.00	30.75	A
ATOM	852	CB	SER	A	119	16.964	19.008	52.833	1.00	29.12	A
ATOM	853	OG	SER	A	119	17.579	19.128	54.104	1.00	36.48	A
ATOM	854	C	SER	A	119	16.975	19.678	50.435	1.00	32.09	A
ATOM	855	O	SER	A	119	15.908	20.216	50.129	1.00	31.84	A
ATOM	856	N	LYS	A	120	17.624	18.856	49.618	1.00	30.36	A
ATOM	857	CA	LYS	A	120	17.107	18.570	48.289	1.00	30.72	A
ATOM	858	CB	LYS	A	120	17.676	19.578	47.287	1.00	38.43	A
ATOM	859	CG	LYS	A	120	16.994	20.930	47.343	1.00	46.43	A
ATOM	860	CD	LYS	A	120	17.880	22.088	46.869	1.00	52.37	A
ATOM	861	CE	LYS	A	120	18.370	21.896	45.448	1.00	56.10	A
ATOM	862	NZ	LYS	A	120	19.304	20.736	45.375	1.00	60.72	A
ATOM	863	C	LYS	A	120	17.388	17.155	47.821	1.00	29.34	A
ATOM	864	O	LYS	A	120	18.391	16.553	48.194	1.00	28.06	A
ATOM	865	N	ASN	A	121	16.477	16.640	47.000	1.00	29.70	A
ATOM	866	CA	ASN	A	121	16.559	15.292	46.442	1.00	26.85	A
ATOM	867	CB	ASN	A	121	17.721	15.186	45.450	1.00	25.98	A
ATOM	868	CG	ASN	A	121	17.524	16.069	44.228	1.00	28.59	A
ATOM	869	OD1	ASN	A	121	17.811	17.258	44.259	1.00	28.35	A
ATOM	870	ND2	ASN	A	121	17.012	15.487	43.150	1.00	35.52	A
ATOM	871	C	ASN	A	121	16.679	14.220	47.514	1.00	27.61	A
ATOM	872	O	ASN	A	121	17.759	13.674	47.758	1.00	26.25	A
ATOM	873	N	ILE	A	122	15.542	13.924	48.140	1.00	25.42	A
ATOM	874	CA	ILE	A	122	15.445	12.928	49.195	1.00	26.10	A
ATOM	875	CB	ILE	A	122	14.966	13.564	50.527	1.00	29.13	A
ATOM	876	CG2	ILE	A	122	15.112	12.566	51.662	1.00	25.11	A
ATOM	877	CG1	ILE	A	122	15.761	14.838	50.832	1.00	29.46	A
ATOM	878	CD1	ILE	A	122	17.237	14.610	51.039	1.00	39.15	A
ATOM	879	C	ILE	A	122	14.409	11.877	48.778	1.00	27.62	A
ATOM	880	O	ILE	A	122	13.316	12.220	48.315	1.00	22.25	A
ATOM	881	N	TRP	A	123	14.762	10.605	48.942	1.00	22.91	A
ATOM	882	CA	TRP	A	123	13.873	9.498	48.604	1.00	24.05	A
ATOM	883	CB	TRP	A	123	14.472	8.678	47.440	1.00	20.25	A
ATOM	884	CG	TRP	A	123	13.586	7.580	46.874	1.00	24.25	A
ATOM	885	CD2	TRP	A	123	14.001	6.489	46.040	1.00	23.28	A

ATOM	886	CE2	TRP	A	123	12.844	5.744	45.718	1.00	22.02	A
ATOM	887	CE3	TRP	A	123	15.237	6.072	45.530	1.00	28.91	A
ATOM	888	CD1	TRP	A	123	12.232	7.453	47.015	1.00	25.35	A
ATOM	889	NE1	TRP	A	123	11.779	6.354	46.324	1.00	19.58	A
ATOM	890	CZ2	TRP	A	123	12.887	4.599	44.910	1.00	27.47	A
ATOM	891	CZ3	TRP	A	123	15.279	4.932	44.722	1.00	32.25	A
ATOM	892	CH2	TRP	A	123	14.108	4.211	44.423	1.00	26.71	A
ATOM	893	C	TRP	A	123	13.698	8.626	49.856	1.00	22.34	A
ATOM	894	O	TRP	A	123	14.647	7.997	50.330	1.00	26.32	A
ATOM	895	N	VAL	A	124	12.490	8.628	50.409	1.00	23.58	A
ATOM	896	CA	VAL	A	124	12.172	7.829	51.591	1.00	22.20	A
ATOM	897	CB	VAL	A	124	11.413	8.667	52.631	1.00	25.15	A
ATOM	898	CG1	VAL	A	124	11.131	7.835	53.873	1.00	20.35	A
ATOM	899	CG2	VAL	A	124	12.247	9.893	52.992	1.00	25.49	A
ATOM	900	C	VAL	A	124	11.312	6.691	51.067	1.00	23.52	A
ATOM	901	O	VAL	A	124	10.123	6.859	50.800	1.00	26.28	A
ATOM	902	N	ASP	A	125	11.933	5.526	50.936	1.00	24.15	A
ATOM	903	CA	ASP	A	125	11.282	4.376	50.337	1.00	24.36	A
ATOM	904	CB	ASP	A	125	11.917	4.177	48.954	1.00	25.05	A
ATOM	905	CG	ASP	A	125	11.384	2.974	48.221	1.00	23.53	A
ATOM	906	OD1	ASP	A	125	10.286	3.072	47.643	1.00	27.53	A
ATOM	907	OD2	ASP	A	125	12.073	1.935	48.221	1.00	25.71	A
ATOM	908	C	ASP	A	125	11.322	3.068	51.132	1.00	25.21	A
ATOM	909	O	ASP	A	125	12.304	2.761	51.803	1.00	23.71	A
ATOM	910	N	HIS	A	126	10.236	2.305	51.029	1.00	22.17	A
ATOM	911	CA	HIS	A	126	10.106	1.011	51.691	1.00	24.13	A
ATOM	912	CB	HIS	A	126	10.894	-.050	50.911	1.00	21.17	A
ATOM	913	CG	HIS	A	126	10.170	-.569	49.706	1.00	22.74	A
ATOM	914	CD2	HIS	A	126	9.196	-1.505	49.592	1.00	22.10	A
ATOM	915	ND1	HIS	A	126	10.374	-.073	48.436	1.00	20.08	A
ATOM	916	CE1	HIS	A	126	9.558	-.680	47.592	1.00	24.39	A
ATOM	917	NE2	HIS	A	126	8.832	-1.553	48.269	1.00	22.78	A
ATOM	918	C	HIS	A	126	10.487	.957	53.172	1.00	26.83	A
ATOM	919	O	HIS	A	126	11.261	.093	53.600	1.00	26.93	A
ATOM	920	N	ASN	A	127	9.934	1.873	53.957	1.00	23.93	A
ATOM	921	CA	ASN	A	127	10.202	1.899	55.385	1.00	25.77	A
ATOM	922	CB	ASN	A	127	10.733	3.265	55.807	1.00	22.20	A
ATOM	923	CG	ASN	A	127	11.994	3.642	55.084	1.00	28.34	A
ATOM	924	OD1	ASN	A	127	13.061	3.105	55.365	1.00	28.50	A
ATOM	925	ND2	ASN	A	127	11.881	4.566	54.135	1.00	24.33	A
ATOM	926	C	ASN	A	127	8.909	1.639	56.128	1.00	26.02	A
ATOM	927	O	ASN	A	127	7.827	1.743	55.553	1.00	26.05	A
ATOM	928	N	GLU	A	128	9.022	1.267	57.399	1.00	25.78	A
ATOM	929	CA	GLU	A	128	7.842	1.067	58.222	1.00	27.13	A
ATOM	930	CB	GLU	A	128	7.747	-.352	58.793	1.00	25.77	A
ATOM	931	CG	GLU	A	128	6.516	-.488	59.699	1.00	30.55	A
ATOM	932	CD	GLU	A	128	6.242	-1.902	60.177	1.00	32.29	A
ATOM	933	OE1	GLU	A	128	6.956	-2.835	59.759	1.00	32.33	A
ATOM	934	OE2	GLU	A	128	5.291	-2.071	60.973	1.00	35.24	A
ATOM	935	C	GLU	A	128	7.987	2.077	59.354	1.00	30.60	A
ATOM	936	O	GLU	A	128	8.947	2.028	60.130	1.00	29.16	A
ATOM	937	N	LEU	A	129	7.033	2.999	59.432	1.00	30.78	A
ATOM	938	CA	LEU	A	129	7.061	4.056	60.436	1.00	29.38	A
ATOM	939	CB	LEU	A	129	7.177	5.416	59.743	1.00	24.33	A
ATOM	940	CG	LEU	A	129	8.251	5.507	58.659	1.00	27.94	A
ATOM	941	CD1	LEU	A	129	8.161	6.855	57.981	1.00	31.83	A
ATOM	942	CD2	LEU	A	129	9.633	5.290	59.260	1.00	27.64	A
ATOM	943	C	LEU	A	129	5.793	4.026	61.274	1.00	30.47	A
ATOM	944	O	LEU	A	129	4.684	4.065	60.736	1.00	26.61	A
ATOM	945	N	TYR	A	130	5.961	3.956	62.592	1.00	29.51	A
ATOM	946	CA	TYR	A	130	4.815	3.921	63.489	1.00	30.15	A
ATOM	947	CB	TYR	A	130	4.186	2.524	63.505	1.00	28.51	A
ATOM	948	CG	TYR	A	130	5.049	1.422	64.096	1.00	30.52	A
ATOM	949	CD1	TYR	A	130	5.996	.752	63.325	1.00	34.75	A
ATOM	950	CE1	TYR	A	130	6.747	-.313	63.855	1.00	34.56	A
ATOM	951	CD2	TYR	A	130	4.875	1.017	65.418	1.00	36.59	A
ATOM	952	CE2	TYR	A	130	5.619	-.039	65.963	1.00	37.84	A
ATOM	953	CZ	TYR	A	130	6.548	-.701	65.175	1.00	41.12	A
ATOM	954	OH	TYR	A	130	7.260	-1.760	65.711	1.00	41.48	A

ATOM	955	C	TYR	A	130	5.139	4.337	64.918	1.00	32.48	A
ATOM	956	O	TYR	A	130	6.289	4.301	65.351	1.00	31.10	A
ATOM	957	N	HIS	A	131	4.099	4.747	65.634	1.00	32.83	A
ATOM	958	CA	HIS	A	131	4.206	5.162	67.027	1.00	36.53	A
ATOM	959	CB	HIS	A	131	3.882	6.653	67.190	1.00	32.39	A
ATOM	960	CG	HIS	A	131	4.957	7.572	66.703	1.00	32.96	A
ATOM	961	CD2	HIS	A	131	4.891	8.731	66.002	1.00	34.66	A
ATOM	962	ND1	HIS	A	131	6.290	7.379	66.993	1.00	32.09	A
ATOM	963	CE1	HIS	A	131	6.998	8.379	66.495	1.00	34.22	A
ATOM	964	NE2	HIS	A	131	6.173	9.214	65.890	1.00	34.58	A
ATOM	965	C	HIS	A	131	3.155	4.337	67.758	1.00	37.28	A
ATOM	966	O	HIS	A	131	3.185	3.108	67.728	1.00	41.90	A
ATOM	967	N	SER	A	132	2.203	5.013	68.382	1.00	37.57	A
ATOM	968	CA	SER	A	132	1.146	4.322	69.096	1.00	37.92	A
ATOM	969	CB	SER	A	132	1.672	3.810	70.443	1.00	41.21	A
ATOM	970	OG	SER	A	132	.665	3.096	71.150	1.00	42.70	A
ATOM	971	C	SER	A	132	-.024	5.270	69.323	1.00	38.83	A
ATOM	972	O	SER	A	132	.160	6.487	69.441	1.00	40.44	A
ATOM	973	N	LEU	A	133	-1.228	4.714	69.360	1.00	39.00	A
ATOM	974	CA	LEU	A	133	-2.415	5.511	69.613	1.00	43.28	A
ATOM	975	CB	LEU	A	133	-3.572	5.061	68.712	1.00	41.96	A
ATOM	976	CG	LEU	A	133	-3.542	5.576	67.267	1.00	45.18	A
ATOM	977	CD1	LEU	A	133	-4.727	5.027	66.495	1.00	42.89	A
ATOM	978	CD2	LEU	A	133	-3.578	7.091	67.261	1.00	40.15	A
ATOM	979	C	LEU	A	133	-2.817	5.367	71.081	1.00	45.27	A
ATOM	980	O	LEU	A	133	-3.667	6.105	71.577	1.00	46.89	A
ATOM	981	N	ASN	A	134	-2.183	4.427	71.775	1.00	47.10	A
ATOM	982	CA	ASN	A	134	-2.501	4.174	73.175	1.00	50.08	A
ATOM	983	CB	ASN	A	134	-2.425	2.673	73.456	1.00	53.21	A
ATOM	984	CG	ASN	A	134	-3.352	1.875	72.569	1.00	56.90	A
ATOM	985	OD1	ASN	A	134	-4.556	2.148	72.502	1.00	60.24	A
ATOM	986	ND2	ASN	A	134	-2.803	.883	71.876	1.00	61.36	A
ATOM	987	C	ASN	A	134	-1.613	4.926	74.158	1.00	48.81	A
ATOM	988	O	ASN	A	134	-1.177	4.368	75.165	1.00	53.53	A
ATOM	989	N	VAL	A	135	-1.346	6.191	73.861	1.00	47.53	A
ATOM	990	CA	VAL	A	135	-.531	7.029	74.724	1.00	47.42	A
ATOM	991	CB	VAL	A	135	.952	7.027	74.308	1.00	45.60	A
ATOM	992	CG1	VAL	A	135	1.548	5.659	74.530	1.00	46.15	A
ATOM	993	CG2	VAL	A	135	1.085	7.441	72.850	1.00	46.57	A
ATOM	994	C	VAL	A	135	-1.070	8.442	74.599	1.00	49.70	A
ATOM	995	O	VAL	A	135	-1.886	8.733	73.710	1.00	47.19	A
ATOM	996	N	ASP	A	136	-.642	9.326	75.494	1.00	53.43	A
ATOM	997	CA	ASP	A	136	-1.117	10.693	75.406	1.00	56.97	A
ATOM	998	CB	ASP	A	136	-.408	11.574	76.430	1.00	61.69	A
ATOM	999	CG	ASP	A	136	-.894	12.997	76.374	1.00	70.28	A
ATOM	1000	OD1	ASP	A	136	-2.137	13.176	76.332	1.00	72.94	A
ATOM	1001	OD2	ASP	A	136	-.049	13.930	76.362	1.00	73.76	A
ATOM	1002	C	ASP	A	136	-.820	11.171	73.977	1.00	55.73	A
ATOM	1003	O	ASP	A	136	.076	10.641	73.318	1.00	51.66	A
ATOM	1004	N	LYS	A	137	-1.575	12.157	73.499	1.00	55.69	A
ATOM	1005	CA	LYS	A	137	-1.396	12.671	72.145	1.00	55.91	A
ATOM	1006	CB	LYS	A	137	-2.538	13.616	71.796	1.00	59.20	A
ATOM	1007	CG	LYS	A	137	-3.912	12.937	71.757	1.00	68.01	A
ATOM	1008	CD	LYS	A	137	-5.030	13.932	71.403	1.00	73.15	A
ATOM	1009	CE	LYS	A	137	-4.751	14.670	70.077	1.00	76.69	A
ATOM	1010	NZ	LYS	A	137	-3.569	15.600	70.148	1.00	76.30	A
ATOM	1011	C	LYS	A	137	-.077	13.382	71.886	1.00	55.00	A
ATOM	1012	O	LYS	A	137	.374	13.453	70.737	1.00	52.93	A
ATOM	1013	N	ASP	A	138	.546	13.898	72.944	1.00	52.53	A
ATOM	1014	CA	ASP	A	138	1.814	14.616	72.806	1.00	53.39	A
ATOM	1015	CB	ASP	A	138	1.773	15.899	73.641	1.00	58.02	A
ATOM	1016	CG	ASP	A	138	.508	16.696	73.413	1.00	63.59	A
ATOM	1017	OD1	ASP	A	138	-.107	17.111	74.423	1.00	67.71	A
ATOM	1018	OD2	ASP	A	138	.127	16.905	72.232	1.00	64.27	A
ATOM	1019	C	ASP	A	138	3.047	13.805	73.206	1.00	49.06	A
ATOM	1020	O	ASP	A	138	4.163	14.319	73.178	1.00	49.03	A
ATOM	1021	N	TYR	A	139	2.852	12.550	73.585	1.00	46.10	A
ATOM	1022	CA	TYR	A	139	3.970	11.696	73.978	1.00	45.35	A
ATOM	1023	CB	TYR	A	139	3.455	10.348	74.478	1.00	45.49	A

ATOM	1024	CG	TYR	A	139	4.523	9.530	75.154	1.00	47.10	A
ATOM	1025	CD1	TYR	A	139	5.052	9.924	76.384	1.00	51.00	A
ATOM	1026	CE1	TYR	A	139	6.078	9.197	76.996	1.00	50.44	A
ATOM	1027	CD2	TYR	A	139	5.039	8.387	74.550	1.00	49.04	A
ATOM	1028	CE2	TYR	A	139	6.063	7.654	75.150	1.00	50.03	A
ATOM	1029	CZ	TYR	A	139	6.577	8.069	76.372	1.00	52.01	A
ATOM	1030	OH	TYR	A	139	7.606	7.368	76.961	1.00	55.90	A
ATOM	1031	C	TYR	A	139	4.932	11.478	72.810	1.00	45.22	A
ATOM	1032	O	TYR	A	139	6.156	11.558	72.980	1.00	46.02	A
ATOM	1033	N	TYR	A	140	4.372	11.186	71.633	1.00	44.45	A
ATOM	1034	CA	TYR	A	140	5.150	10.978	70.403	1.00	39.55	A
ATOM	1035	CB	TYR	A	140	4.820	9.629	69.744	1.00	39.19	A
ATOM	1036	CG	TYR	A	140	5.156	8.393	70.554	1.00	40.56	A
ATOM	1037	CD1	TYR	A	140	4.177	7.446	70.852	1.00	39.59	A
ATOM	1038	CE1	TYR	A	140	4.486	6.278	71.565	1.00	40.07	A
ATOM	1039	CD2	TYR	A	140	6.460	8.150	70.991	1.00	41.32	A
ATOM	1040	CE2	TYR	A	140	6.780	6.993	71.702	1.00	41.22	A
ATOM	1041	CZ	TYR	A	140	5.787	6.060	71.986	1.00	42.33	A
ATOM	1042	OH	TYR	A	140	6.103	4.907	72.685	1.00	47.99	A
ATOM	1043	C	TYR	A	140	4.688	12.081	69.460	1.00	38.73	A
ATOM	1044	O	TYR	A	140	3.590	12.623	69.629	1.00	39.43	A
ATOM	1045	N	ASP	A	141	5.499	12.414	68.464	1.00	38.05	A
ATOM	1046	CA	ASP	A	141	5.100	13.455	67.530	1.00	36.47	A
ATOM	1047	CB	ASP	A	141	6.093	14.615	67.567	1.00	36.93	A
ATOM	1048	CG	ASP	A	141	5.530	15.873	66.951	1.00	35.68	A
ATOM	1049	OD1	ASP	A	141	4.330	16.135	67.170	1.00	39.66	A
ATOM	1050	OD2	ASP	A	141	6.279	16.603	66.258	1.00	42.79	A
ATOM	1051	C	ASP	A	141	4.939	12.928	66.104	1.00	35.35	A
ATOM	1052	O	ASP	A	141	4.256	11.930	65.879	1.00	37.04	A
ATOM	1053	N	GLY	A	142	5.579	13.580	65.144	1.00	34.72	A
ATOM	1054	CA	GLY	A	142	5.425	13.160	63.761	1.00	36.57	A
ATOM	1055	C	GLY	A	142	6.075	11.864	63.310	1.00	32.81	A
ATOM	1056	O	GLY	A	142	6.990	11.344	63.950	1.00	31.53	A
ATOM	1057	N	LEU	A	143	5.582	11.334	62.195	1.00	29.42	A
ATOM	1058	CA	LEU	A	143	6.143	10.120	61.629	1.00	29.32	A
ATOM	1059	CB	LEU	A	143	5.027	9.187	61.159	1.00	29.42	A
ATOM	1060	CG	LEU	A	143	4.321	8.441	62.294	1.00	30.37	A
ATOM	1061	CD1	LEU	A	143	3.075	7.761	61.777	1.00	27.05	A
ATOM	1062	CD2	LEU	A	143	5.287	7.432	62.912	1.00	31.74	A
ATOM	1063	C	LEU	A	143	7.038	10.538	60.465	1.00	29.38	A
ATOM	1064	O	LEU	A	143	8.105	9.960	60.248	1.00	33.45	A
ATOM	1065	N	PHE	A	144	6.597	11.555	59.728	1.00	28.68	A
ATOM	1066	CA	PHE	A	144	7.351	12.087	58.593	1.00	28.57	A
ATOM	1067	CB	PHE	A	144	7.024	11.329	57.298	1.00	27.97	A
ATOM	1068	CG	PHE	A	144	7.737	11.865	56.080	1.00	28.12	A
ATOM	1069	CD1	PHE	A	144	7.017	12.404	55.015	1.00	26.49	A
ATOM	1070	CD2	PHE	A	144	9.126	11.822	55.990	1.00	26.00	A
ATOM	1071	CE1	PHE	A	144	7.672	12.888	53.877	1.00	27.00	A
ATOM	1072	CE2	PHE	A	144	9.787	12.306	54.853	1.00	29.95	A
ATOM	1073	CZ	PHE	A	144	9.057	12.837	53.799	1.00	22.95	A
ATOM	1074	C	PHE	A	144	6.974	13.544	58.429	1.00	27.68	A
ATOM	1075	O	PHE	A	144	5.971	13.860	57.795	1.00	30.30	A
ATOM	1076	N	ASP	A	145	7.773	14.424	59.019	1.00	28.39	A
ATOM	1077	CA	ASP	A	145	7.523	15.850	58.944	1.00	27.85	A
ATOM	1078	CB	ASP	A	145	7.474	16.465	60.342	1.00	31.05	A
ATOM	1079	CG	ASP	A	145	6.311	15.954	61.163	1.00	34.74	A
ATOM	1080	OD1	ASP	A	145	5.348	15.413	60.575	1.00	33.87	A
ATOM	1081	OD2	ASP	A	145	6.346	16.106	62.403	1.00	39.68	A
ATOM	1082	C	ASP	A	145	8.593	16.546	58.120	1.00	30.73	A
ATOM	1083	O	ASP	A	145	9.751	16.126	58.090	1.00	28.20	A
ATOM	1084	N	VAL	A	146	8.193	17.622	57.459	1.00	27.94	A
ATOM	1085	CA	VAL	A	146	9.098	18.380	56.616	1.00	28.85	A
ATOM	1086	CB	VAL	A	146	8.838	18.083	55.120	1.00	26.13	A
ATOM	1087	CG1	VAL	A	146	9.886	18.751	54.269	1.00	28.77	A
ATOM	1088	CG2	VAL	A	146	8.815	16.590	54.876	1.00	21.83	A
ATOM	1089	C	VAL	A	146	8.819	19.849	56.871	1.00	30.20	A
ATOM	1090	O	VAL	A	146	7.663	20.272	56.866	1.00	28.96	A
ATOM	1091	N	LYS	A	147	9.869	20.627	57.112	1.00	29.62	A
ATOM	1092	CA	LYS	A	147	9.692	22.056	57.342	1.00	32.71	A

ATOM	1093	CB	LYS	A	147	9.805	22.382	58.832	1.00	35.71	A
ATOM	1094	CG	LYS	A	147	11.109	21.933	59.462	1.00	43.55	A
ATOM	1095	CD	LYS	A	147	11.288	22.496	60.869	1.00	51.92	A
ATOM	1096	CE	LYS	A	147	10.175	22.065	61.807	1.00	53.62	A
ATOM	1097	NZ	LYS	A	147	10.141	20.580	61.992	1.00	60.62	A
ATOM	1098	C	LYS	A	147	10.713	22.875	56.560	1.00	31.08	A
ATOM	1099	O	LYS	A	147	11.719	22.350	56.095	1.00	29.04	A
ATOM	1100	N	ARG	A	148	10.436	24.166	56.423	1.00	28.98	A
ATOM	1101	CA	ARG	A	148	11.323	25.074	55.712	1.00	33.84	A
ATOM	1102	CB	ARG	A	148	12.708	25.125	56.376	1.00	38.29	A
ATOM	1103	CG	ARG	A	148	12.748	25.665	57.803	1.00	47.09	A
ATOM	1104	CD	ARG	A	148	14.088	26.396	58.040	1.00	53.95	A
ATOM	1105	NE	ARG	A	148	14.180	27.572	57.158	1.00	64.90	A
ATOM	1106	CZ	ARG	A	148	15.231	27.884	56.393	1.00	65.79	A
ATOM	1107	NH1	ARG	A	148	15.196	28.976	55.629	1.00	63.48	A
ATOM	1108	NH2	ARG	A	148	16.317	27.117	56.392	1.00	66.14	A
ATOM	1109	C	ARG	A	148	11.489	24.725	54.236	1.00	33.94	A
ATOM	1110	O	ARG	A	148	10.599	24.135	53.624	1.00	28.88	A
ATOM	1111	N	ASP	A	149	12.640	25.096	53.675	1.00	33.28	A
ATOM	1112	CA	ASP	A	149	12.936	24.883	52.262	1.00	34.04	A
ATOM	1113	CB	ASP	A	149	13.863	25.995	51.736	1.00	35.92	A
ATOM	1114	CG	ASP	A	149	15.043	26.274	52.660	1.00	36.37	A
ATOM	1115	OD1	ASP	A	149	15.985	26.956	52.207	1.00	42.00	A
ATOM	1116	OD2	ASP	A	149	15.038	25.837	53.831	1.00	36.30	A
ATOM	1117	C	ASP	A	149	13.514	23.535	51.874	1.00	35.09	A
ATOM	1118	O	ASP	A	149	14.699	23.413	51.572	1.00	32.16	A
ATOM	1119	N	ALA	A	150	12.660	22.521	51.867	1.00	33.19	A
ATOM	1120	CA	ALA	A	150	13.076	21.186	51.483	1.00	30.91	A
ATOM	1121	CB	ALA	A	150	12.658	20.189	52.544	1.00	32.36	A
ATOM	1122	C	ALA	A	150	12.341	20.931	50.176	1.00	32.37	A
ATOM	1123	O	ALA	A	150	11.154	21.224	50.075	1.00	33.85	A
ATOM	1124	N	GLU	A	151	13.030	20.408	49.168	1.00	29.34	A
ATOM	1125	CA	GLU	A	151	12.368	20.165	47.895	1.00	28.53	A
ATOM	1126	CB	GLU	A	151	12.465	21.423	47.016	1.00	33.48	A
ATOM	1127	CG	GLU	A	151	13.850	22.037	46.934	1.00	39.59	A
ATOM	1128	CD	GLU	A	151	13.814	23.512	46.541	1.00	42.23	A
ATOM	1129	OE1	GLU	A	151	13.173	23.867	45.528	1.00	41.31	A
ATOM	1130	OE2	GLU	A	151	14.432	24.322	47.253	1.00	49.30	A
ATOM	1131	C	GLU	A	151	12.852	18.940	47.133	1.00	28.36	A
ATOM	1132	O	GLU	A	151	13.921	18.400	47.419	1.00	24.68	A
ATOM	1133	N	TYR	A	152	12.050	18.513	46.159	1.00	23.56	A
ATOM	1134	CA	TYR	A	152	12.357	17.341	45.339	1.00	25.25	A
ATOM	1135	CB	TYR	A	152	13.675	17.552	44.584	1.00	26.27	A
ATOM	1136	CG	TYR	A	152	13.638	18.765	43.680	1.00	31.30	A
ATOM	1137	CD1	TYR	A	152	12.773	18.815	42.591	1.00	34.20	A
ATOM	1138	CE1	TYR	A	152	12.694	19.943	41.779	1.00	37.80	A
ATOM	1139	CD2	TYR	A	152	14.435	19.879	43.939	1.00	36.18	A
ATOM	1140	CE2	TYR	A	152	14.368	21.020	43.135	1.00	33.13	A
ATOM	1141	CZ	TYR	A	152	13.493	21.045	42.057	1.00	41.06	A
ATOM	1142	OH	TYR	A	152	13.390	22.165	41.254	1.00	43.95	A
ATOM	1143	C	TYR	A	152	12.438	16.113	46.237	1.00	23.72	A
ATOM	1144	O	TYR	A	152	13.484	15.494	46.387	1.00	23.91	A
ATOM	1145	N	ILE	A	153	11.301	15.776	46.831	1.00	22.55	A
ATOM	1146	CA	ILE	A	153	11.195	14.655	47.748	1.00	20.42	A
ATOM	1147	CB	ILE	A	153	10.786	15.150	49.151	1.00	22.15	A
ATOM	1148	CG2	ILE	A	153	10.616	13.968	50.095	1.00	22.58	A
ATOM	1149	CG1	ILE	A	153	11.824	16.143	49.672	1.00	25.33	A
ATOM	1150	CD1	ILE	A	153	11.405	16.834	50.953	1.00	31.14	A
ATOM	1151	C	ILE	A	153	10.148	13.646	47.301	1.00	22.78	A
ATOM	1152	O	ILE	A	153	9.041	14.020	46.924	1.00	22.11	A
ATOM	1153	N	THR	A	154	10.503	12.369	47.341	1.00	23.28	A
ATOM	1154	CA	THR	A	154	9.561	11.318	46.988	1.00	22.67	A
ATOM	1155	CB	THR	A	154	10.007	10.525	45.742	1.00	22.57	A
ATOM	1156	OG1	THR	A	154	9.988	11.383	44.590	1.00	18.77	A
ATOM	1157	CG2	THR	A	154	9.074	9.330	45.517	1.00	15.72	A
ATOM	1158	C	THR	A	154	9.447	10.372	48.179	1.00	24.91	A
ATOM	1159	O	THR	A	154	10.447	9.858	48.687	1.00	23.13	A
ATOM	1160	N	PHE	A	155	8.213	10.176	48.627	1.00	24.73	A
ATOM	1161	CA	PHE	A	155	7.883	9.311	49.759	1.00	22.77	A

ATOM	1162	CB	PHE	A	155	7.011	10.094	50.740	1.00	19.95	A
ATOM	1163	CG	PHE	A	155	6.789	9.409	52.056	1.00	21.32	A
ATOM	1164	CD1	PHE	A	155	7.778	9.408	53.028	1.00	19.84	A
ATOM	1165	CD2	PHE	A	155	5.570	8.800	52.336	1.00	22.47	A
ATOM	1166	CE1	PHE	A	155	7.554	8.814	54.270	1.00	23.98	A
ATOM	1167	CE2	PHE	A	155	5.336	8.204	53.570	1.00	24.73	A
ATOM	1168	CZ	PHE	A	155	6.331	8.212	54.541	1.00	27.83	A
ATOM	1169	C	PHE	A	155	7.084	8.177	49.126	1.00	23.32	A
ATOM	1170	O	PHE	A	155	5.938	8.379	48.735	1.00	21.46	A
ATOM	1171	N	SER	A	156	7.679	6.993	49.027	1.00	19.49	A
ATOM	1172	CA	SER	A	156	7.003	5.880	48.374	1.00	18.64	A
ATOM	1173	CB	SER	A	156	7.479	5.789	46.919	1.00	18.87	A
ATOM	1174	OG	SER	A	156	8.869	5.491	46.854	1.00	22.30	A
ATOM	1175	C	SER	A	156	7.151	4.501	49.018	1.00	22.30	A
ATOM	1176	O	SER	A	156	8.145	4.210	49.663	1.00	21.34	A
ATOM	1177	N	TRP	A	157	6.142	3.661	48.804	1.00	18.11	A
ATOM	1178	CA	TRP	A	157	6.116	2.292	49.306	1.00	22.75	A
ATOM	1179	CB	TRP	A	157	7.126	1.439	48.539	1.00	18.56	A
ATOM	1180	CG	TRP	A	157	6.873	1.390	47.061	1.00	22.47	A
ATOM	1181	CD2	TRP	A	157	5.899	.588	46.382	1.00	20.49	A
ATOM	1182	CE2	TRP	A	157	6.021	.861	45.003	1.00	22.41	A
ATOM	1183	CE3	TRP	A	157	4.930	-.336	46.806	1.00	23.66	A
ATOM	1184	CD1	TRP	A	157	7.525	2.099	46.093	1.00	21.42	A
ATOM	1185	NE1	TRP	A	157	7.021	1.785	44.855	1.00	22.12	A
ATOM	1186	CZ2	TRP	A	157	5.212	.242	44.039	1.00	22.42	A
ATOM	1187	CZ3	TRP	A	157	4.122	-.952	45.847	1.00	22.99	A
ATOM	1188	CH2	TRP	A	157	4.273	-.657	44.478	1.00	21.35	A
ATOM	1189	C	TRP	A	157	6.353	2.133	50.807	1.00	23.21	A
ATOM	1190	O	TRP	A	157	6.886	1.121	51.252	1.00	24.46	A
ATOM	1191	N	ASN	A	158	5.946	3.135	51.577	1.00	23.79	A
ATOM	1192	CA	ASN	A	158	6.095	3.102	53.019	1.00	23.96	A
ATOM	1193	CB	ASN	A	158	6.421	4.502	53.542	1.00	26.82	A
ATOM	1194	CG	ASN	A	158	7.720	5.045	52.982	1.00	25.52	A
ATOM	1195	OD1	ASN	A	158	8.797	4.536	53.290	1.00	27.31	A
ATOM	1196	ND2	ASN	A	158	7.622	6.079	52.148	1.00	22.07	A
ATOM	1197	C	ASN	A	158	4.827	2.594	53.711	1.00	24.17	A
ATOM	1198	O	ASN	A	158	3.715	2.736	53.200	1.00	20.69	A
ATOM	1199	N	TYR	A	159	5.015	1.988	54.879	1.00	23.03	A
ATOM	1200	CA	TYR	A	159	3.908	1.492	55.687	1.00	26.62	A
ATOM	1201	CB	TYR	A	159	4.138	.016	56.057	1.00	29.69	A
ATOM	1202	CG	TYR	A	159	3.065	-.598	56.939	1.00	31.18	A
ATOM	1203	CD1	TYR	A	159	1.745	-.142	56.898	1.00	29.94	A
ATOM	1204	CE1	TYR	A	159	.753	-.721	57.694	1.00	32.17	A
ATOM	1205	CD2	TYR	A	159	3.367	-1.654	57.800	1.00	32.52	A
ATOM	1206	CE2	TYR	A	159	2.389	-2.242	58.595	1.00	30.15	A
ATOM	1207	CZ	TYR	A	159	1.083	-1.773	58.542	1.00	35.62	A
ATOM	1208	OH	TYR	A	159	.115	-2.346	59.342	1.00	31.72	A
ATOM	1209	C	TYR	A	159	3.890	2.384	56.931	1.00	24.38	A
ATOM	1210	O	TYR	A	159	4.683	2.203	57.855	1.00	28.88	A
ATOM	1211	N	VAL	A	160	2.995	3.366	56.925	1.00	27.33	A
ATOM	1212	CA	VAL	A	160	2.871	4.329	58.018	1.00	24.98	A
ATOM	1213	CB	VAL	A	160	2.834	5.767	57.453	1.00	26.64	A
ATOM	1214	CG1	VAL	A	160	2.954	6.786	58.575	1.00	20.10	A
ATOM	1215	CG2	VAL	A	160	3.957	5.938	56.437	1.00	22.68	A
ATOM	1216	C	VAL	A	160	1.598	4.052	58.807	1.00	25.79	A
ATOM	1217	O	VAL	A	160	.498	4.082	58.255	1.00	24.23	A
ATOM	1218	N	HIS	A	161	1.738	3.798	60.107	1.00	26.86	A
ATOM	1219	CA	HIS	A	161	.564	3.468	60.906	1.00	26.55	A
ATOM	1220	CB	HIS	A	161	.237	1.987	60.694	1.00	28.15	A
ATOM	1221	CG	HIS	A	161	1.332	1.064	61.133	1.00	25.47	A
ATOM	1222	CD2	HIS	A	161	2.419	.592	60.476	1.00	31.16	A
ATOM	1223	ND1	HIS	A	161	1.416	.565	62.415	1.00	29.56	A
ATOM	1224	CE1	HIS	A	161	2.505	-.175	62.529	1.00	26.92	A
ATOM	1225	NE2	HIS	A	161	3.133	-.175	61.367	1.00	33.10	A
ATOM	1226	C	HIS	A	161	.685	3.743	62.407	1.00	29.14	A
ATOM	1227	O	HIS	A	161	1.778	3.942	62.934	1.00	24.01	A
ATOM	1228	N	ASP	A	162	-.463	3.748	63.078	1.00	29.26	A
ATOM	1229	CA	ASP	A	162	-.533	3.956	64.521	1.00	29.89	A
ATOM	1230	CB	ASP	A	162	.033	2.716	65.219	1.00	30.61	A

ATOM	1231	CG	ASP	A	162	-.848	1.494	65.018	1.00	33.79	A
ATOM	1232	OD1	ASP	A	162	-1.907	1.428	65.669	1.00	36.69	A
ATOM	1233	OD2	ASP	A	162	-.506	.610	64.198	1.00	35.07	A
ATOM	1234	C	ASP	A	162	.141	5.221	65.035	1.00	27.49	A
ATOM	1235	O	ASP	A	162	1.222	5.173	65.611	1.00	23.89	A
ATOM	1236	N	GLY	A	163	-.517	6.355	64.820	1.00	30.06	A
ATOM	1237	CA	GLY	A	163	.018	7.629	65.269	1.00	28.38	A
ATOM	1238	C	GLY	A	163	-1.049	8.706	65.284	1.00	27.77	A
ATOM	1239	O	GLY	A	163	-1.975	8.682	64.469	1.00	27.89	A
ATOM	1240	N	TRP	A	164	-.929	9.646	66.218	1.00	28.63	A
ATOM	1241	CA	TRP	A	164	-1.888	10.738	66.339	1.00	30.87	A
ATOM	1242	CB	TRP	A	164	-1.794	11.405	67.719	1.00	34.30	A
ATOM	1243	CG	TRP	A	164	-2.443	10.641	68.827	1.00	39.32	A
ATOM	1244	CD2	TRP	A	164	-3.832	10.647	69.167	1.00	39.66	A
ATOM	1245	CE2	TRP	A	164	-4.000	9.761	70.255	1.00	41.88	A
ATOM	1246	CE3	TRP	A	164	-4.955	11.314	68.657	1.00	40.79	A
ATOM	1247	CD1	TRP	A	164	-1.838	9.778	69.699	1.00	41.86	A
ATOM	1248	NE1	TRP	A	164	-2.768	9.246	70.561	1.00	38.96	A
ATOM	1249	CZ2	TRP	A	164	-5.251	9.524	70.844	1.00	44.87	A
ATOM	1250	CZ3	TRP	A	164	-6.200	11.080	69.243	1.00	41.66	A
ATOM	1251	CH2	TRP	A	164	-6.337	10.192	70.324	1.00	43.03	A
ATOM	1252	C	TRP	A	164	-1.668	11.806	65.274	1.00	31.11	A
ATOM	1253	O	TRP	A	164	-2.618	12.302	64.672	1.00	30.17	A
ATOM	1254	N	LYS	A	165	-.408	12.163	65.061	1.00	31.31	A
ATOM	1255	CA	LYS	A	165	-.043	13.190	64.087	1.00	35.52	A
ATOM	1256	CB	LYS	A	165	.638	14.351	64.817	1.00	38.84	A
ATOM	1257	CG	LYS	A	165	-.239	15.008	65.884	1.00	37.87	A
ATOM	1258	CD	LYS	A	165	.587	15.633	67.005	1.00	36.99	A
ATOM	1259	CE	LYS	A	165	1.160	14.563	67.929	1.00	38.51	A
ATOM	1260	NZ	LYS	A	165	2.139	15.116	68.915	1.00	40.83	A
ATOM	1261	C	LYS	A	165	.911	12.555	63.084	1.00	34.77	A
ATOM	1262	O	LYS	A	165	2.096	12.403	63.357	1.00	41.22	A
ATOM	1263	N	SER	A	166	.397	12.192	61.918	1.00	35.05	A
ATOM	1264	CA	SER	A	166	1.213	11.519	60.915	1.00	30.67	A
ATOM	1265	CB	SER	A	166	.305	10.841	59.892	1.00	32.43	A
ATOM	1266	OG	SER	A	166	1.062	10.019	59.024	1.00	34.88	A
ATOM	1267	C	SER	A	166	2.281	12.323	60.175	1.00	27.61	A
ATOM	1268	O	SER	A	166	3.478	12.102	60.375	1.00	27.85	A
ATOM	1269	N	MET	A	167	1.854	13.240	59.310	1.00	26.84	A
ATOM	1270	CA	MET	A	167	2.800	14.017	58.516	1.00	26.21	A
ATOM	1271	CB	MET	A	167	2.871	13.433	57.104	1.00	22.66	A
ATOM	1272	CG	MET	A	167	2.988	11.920	57.074	1.00	26.90	A
ATOM	1273	SD	MET	A	167	3.002	11.219	55.402	1.00	29.71	A
ATOM	1274	CE	MET	A	167	1.241	11.059	55.084	1.00	25.81	A
ATOM	1275	C	MET	A	167	2.475	15.503	58.428	1.00	24.87	A
ATOM	1276	O	MET	A	167	1.401	15.895	57.962	1.00	24.54	A
ATOM	1277	N	LEU	A	168	3.422	16.325	58.864	1.00	21.39	A
ATOM	1278	CA	LEU	A	168	3.252	17.765	58.829	1.00	25.19	A
ATOM	1279	CB	LEU	A	168	3.491	18.350	60.222	1.00	28.68	A
ATOM	1280	CG	LEU	A	168	3.277	19.857	60.420	1.00	29.26	A
ATOM	1281	CD1	LEU	A	168	1.791	20.171	60.366	1.00	29.16	A
ATOM	1282	CD2	LEU	A	168	3.837	20.293	61.766	1.00	29.51	A
ATOM	1283	C	LEU	A	168	4.239	18.375	57.838	1.00	24.80	A
ATOM	1284	O	LEU	A	168	5.451	18.310	58.040	1.00	25.06	A
ATOM	1285	N	MET	A	169	3.718	18.952	56.762	1.00	22.77	A
ATOM	1286	CA	MET	A	169	4.559	19.596	55.755	1.00	20.49	A
ATOM	1287	CB	MET	A	169	4.099	19.204	54.345	1.00	23.72	A
ATOM	1288	CG	MET	A	169	3.801	17.707	54.136	1.00	30.83	A
ATOM	1289	SD	MET	A	169	5.239	16.624	54.241	1.00	41.13	A
ATOM	1290	CE	MET	A	169	4.890	15.732	55.701	1.00	31.45	A
ATOM	1291	C	MET	A	169	4.367	21.098	55.967	1.00	22.82	A
ATOM	1292	O	MET	A	169	3.346	21.658	55.568	1.00	24.99	A
ATOM	1293	N	GLY	A	170	5.346	21.746	56.594	1.00	27.82	A
ATOM	1294	CA	GLY	A	170	5.241	23.168	56.882	1.00	22.52	A
ATOM	1295	C	GLY	A	170	4.907	23.319	58.359	1.00	31.59	A
ATOM	1296	O	GLY	A	170	3.799	22.983	58.782	1.00	28.68	A
ATOM	1297	N	SER	A	171	5.863	23.826	59.138	1.00	31.18	A
ATOM	1298	CA	SER	A	171	5.718	23.992	60.584	1.00	31.00	A
ATOM	1299	CB	SER	A	171	7.051	24.447	61.190	1.00	32.83	A

ATOM	1300	OG	SER	A	171	7.540	25.613	60.542	1.00	37.76	A
ATOM	1301	C	SER	A	171	4.611	24.914	61.077	1.00	34.69	A
ATOM	1302	O	SER	A	171	4.056	24.694	62.161	1.00	35.28	A
ATOM	1303	N	SER	A	172	4.289	25.943	60.301	1.00	29.57	A
ATOM	1304	CA	SER	A	172	3.247	26.893	60.687	1.00	29.41	A
ATOM	1305	CB	SER	A	172	3.811	27.950	61.638	1.00	31.41	A
ATOM	1306	OG	SER	A	172	4.700	28.809	60.940	1.00	37.80	A
ATOM	1307	C	SER	A	172	2.721	27.601	59.454	1.00	25.61	A
ATOM	1308	O	SER	A	172	3.278	27.460	58.372	1.00	23.52	A
ATOM	1309	N	ASP	A	173	1.660	28.380	59.625	1.00	26.67	A
ATOM	1310	CA	ASP	A	173	1.091	29.111	58.504	1.00	26.29	A
ATOM	1311	CB	ASP	A	173	-.242	29.765	58.892	1.00	26.54	A
ATOM	1312	CG	ASP	A	173	-1.401	28.770	58.934	1.00	27.00	A
ATOM	1313	OD1	ASP	A	173	-1.240	27.623	58.454	1.00	30.68	A
ATOM	1314	OD2	ASP	A	173	-2.486	29.145	59.430	1.00	26.14	A
ATOM	1315	C	ASP	A	173	2.056	30.167	57.973	1.00	28.67	A
ATOM	1316	O	ASP	A	173	1.736	30.882	57.023	1.00	25.82	A
ATOM	1317	N	SER	A	174	3.236	30.259	58.588	1.00	27.18	A
ATOM	1318	CA	SER	A	174	4.257	31.218	58.163	1.00	29.22	A
ATOM	1319	CB	SER	A	174	4.763	32.033	59.350	1.00	30.08	A
ATOM	1320	OG	SER	A	174	3.831	33.039	59.679	1.00	40.69	A
ATOM	1321	C	SER	A	174	5.451	30.555	57.490	1.00	28.72	A
ATOM	1322	O	SER	A	174	6.331	31.239	56.987	1.00	25.79	A
ATOM	1323	N	ASP	A	175	5.484	29.226	57.497	1.00	30.40	A
ATOM	1324	CA	ASP	A	175	6.581	28.486	56.878	1.00	29.66	A
ATOM	1325	CB	ASP	A	175	6.643	27.067	57.461	1.00	27.08	A
ATOM	1326	CG	ASP	A	175	7.848	26.279	56.971	1.00	28.17	A
ATOM	1327	OD1	ASP	A	175	8.041	25.135	57.431	1.00	31.07	A
ATOM	1328	OD2	ASP	A	175	8.595	26.796	56.127	1.00	32.39	A
ATOM	1329	C	ASP	A	175	6.323	28.450	55.368	1.00	31.71	A
ATOM	1330	O	ASP	A	175	6.042	27.397	54.795	1.00	30.14	A
ATOM	1331	N	ASN	A	176	6.430	29.618	54.743	1.00	26.30	A
ATOM	1332	CA	ASN	A	176	6.177	29.783	53.318	1.00	32.20	A
ATOM	1333	CB	ASN	A	176	5.755	31.229	53.032	1.00	33.97	A
ATOM	1334	CG	ASN	A	176	5.251	31.422	51.607	1.00	42.98	A
ATOM	1335	OD1	ASN	A	176	5.516	30.601	50.727	1.00	45.93	A
ATOM	1336	ND2	ASN	A	176	4.529	32.518	51.371	1.00	43.00	A
ATOM	1337	C	ASN	A	176	7.346	29.424	52.407	1.00	35.48	A
ATOM	1338	O	ASN	A	176	8.195	30.263	52.125	1.00	35.96	A
ATOM	1339	N	TYR	A	177	7.385	28.177	51.947	1.00	32.51	A
ATOM	1340	CA	TYR	A	177	8.433	27.717	51.034	1.00	33.06	A
ATOM	1341	CB	TYR	A	177	9.563	27.028	51.807	1.00	33.51	A
ATOM	1342	CG	TYR	A	177	10.354	27.946	52.730	1.00	44.22	A
ATOM	1343	CD1	TYR	A	177	11.357	28.783	52.233	1.00	48.10	A
ATOM	1344	CE1	TYR	A	177	12.091	29.623	53.088	1.00	52.05	A
ATOM	1345	CD2	TYR	A	177	10.101	27.974	54.106	1.00	47.83	A
ATOM	1346	CE2	TYR	A	177	10.824	28.809	54.966	1.00	49.35	A
ATOM	1347	CZ	TYR	A	177	11.818	29.628	54.451	1.00	53.24	A
ATOM	1348	OH	TYR	A	177	12.550	30.445	55.300	1.00	60.96	A
ATOM	1349	C	TYR	A	177	7.757	26.737	50.074	1.00	31.78	A
ATOM	1350	O	TYR	A	177	6.876	25.978	50.481	1.00	28.52	A
ATOM	1351	N	ASN	A	178	8.152	26.752	48.804	1.00	31.16	A
ATOM	1352	CA	ASN	A	178	7.526	25.865	47.830	1.00	31.30	A
ATOM	1353	CB	ASN	A	178	7.679	26.433	46.425	1.00	33.82	A
ATOM	1354	CG	ASN	A	178	6.705	25.815	45.453	1.00	35.23	A
ATOM	1355	OD1	ASN	A	178	5.490	25.883	45.651	1.00	41.19	A
ATOM	1356	ND2	ASN	A	178	7.226	25.205	44.398	1.00	40.46	A
ATOM	1357	C	ASN	A	178	8.046	24.429	47.862	1.00	28.89	A
ATOM	1358	O	ASN	A	178	8.767	23.990	46.966	1.00	30.23	A
ATOM	1359	N	ARG	A	179	7.674	23.698	48.901	1.00	24.52	A
ATOM	1360	CA	ARG	A	179	8.090	22.317	49.022	1.00	23.95	A
ATOM	1361	CB	ARG	A	179	7.663	21.777	50.387	1.00	22.75	A
ATOM	1362	CG	ARG	A	179	8.445	22.393	51.557	1.00	23.98	A
ATOM	1363	CD	ARG	A	179	7.842	22.017	52.889	1.00	20.45	A
ATOM	1364	NE	ARG	A	179	6.643	22.799	53.183	1.00	23.33	A
ATOM	1365	CZ	ARG	A	179	6.654	24.012	53.735	1.00	24.62	A
ATOM	1366	NH1	ARG	A	179	5.511	24.650	53.959	1.00	18.40	A
ATOM	1367	NH2	ARG	A	179	7.807	24.582	54.078	1.00	20.03	A
ATOM	1368	C	ARG	A	179	7.449	21.511	47.888	1.00	25.11	A

ATOM	1369	O	ARG	A	179	6.295	21.738	47.537	1.00	25.89	A
ATOM	1370	N	THR	A	180	8.213	20.587	47.313	1.00	24.86	A
ATOM	1371	CA	THR	A	180	7.743	19.734	46.222	1.00	21.91	A
ATOM	1372	CB	THR	A	180	8.564	19.975	44.945	1.00	21.28	A
ATOM	1373	OG1	THR	A	180	9.936	20.191	45.291	1.00	20.74	A
ATOM	1374	CG2	THR	A	180	8.032	21.183	44.202	1.00	24.11	A
ATOM	1375	C	THR	A	180	7.887	18.278	46.655	1.00	23.18	A
ATOM	1376	O	THR	A	180	8.994	17.750	46.731	1.00	21.52	A
ATOM	1377	N	ILE	A	181	6.757	17.630	46.922	1.00	20.71	A
ATOM	1378	CA	ILE	A	181	6.760	16.258	47.404	1.00	20.88	A
ATOM	1379	CB	ILE	A	181	6.428	16.213	48.918	1.00	27.25	A
ATOM	1380	CG2	ILE	A	181	6.593	14.790	49.450	1.00	24.93	A
ATOM	1381	CG1	ILE	A	181	7.349	17.164	49.684	1.00	26.98	A
ATOM	1382	CD1	ILE	A	181	7.061	17.208	51.173	1.00	34.19	A
ATOM	1383	C	ILE	A	181	5.781	15.330	46.698	1.00	23.47	A
ATOM	1384	O	ILE	A	181	4.627	15.691	46.449	1.00	19.50	A
ATOM	1385	N	THR	A	182	6.247	14.123	46.397	1.00	19.55	A
ATOM	1386	CA	THR	A	182	5.407	13.124	45.754	1.00	19.81	A
ATOM	1387	CB	THR	A	182	6.073	12.520	44.492	1.00	19.81	A
ATOM	1388	OG1	THR	A	182	6.289	13.541	43.508	1.00	21.49	A
ATOM	1389	CG2	THR	A	182	5.184	11.427	43.902	1.00	16.68	A
ATOM	1390	C	THR	A	182	5.169	11.991	46.738	1.00	19.56	A
ATOM	1391	O	THR	A	182	6.119	11.472	47.322	1.00	22.28	A
ATOM	1392	N	PHE	A	183	3.904	11.621	46.930	1.00	18.22	A
ATOM	1393	CA	PHE	A	183	3.535	10.513	47.817	1.00	18.45	A
ATOM	1394	CB	PHE	A	183	2.527	10.941	48.893	1.00	19.28	A
ATOM	1395	CG	PHE	A	183	3.003	12.030	49.807	1.00	17.96	A
ATOM	1396	CD1	PHE	A	183	2.992	13.356	49.400	1.00	22.55	A
ATOM	1397	CD2	PHE	A	183	3.394	11.734	51.111	1.00	25.42	A
ATOM	1398	CE1	PHE	A	183	3.356	14.377	50.282	1.00	24.46	A
ATOM	1399	CE2	PHE	A	183	3.760	12.746	52.001	1.00	20.04	A
ATOM	1400	CZ	PHE	A	183	3.738	14.071	51.584	1.00	23.60	A
ATOM	1401	C	PHE	A	183	2.843	9.435	46.971	1.00	20.32	A
ATOM	1402	O	PHE	A	183	1.753	9.673	46.439	1.00	19.96	A
ATOM	1403	N	HIS	A	184	3.445	8.259	46.837	1.00	17.34	A
ATOM	1404	CA	HIS	A	184	2.791	7.217	46.060	1.00	20.75	A
ATOM	1405	CB	HIS	A	184	3.159	7.339	44.569	1.00	20.78	A
ATOM	1406	CG	HIS	A	184	4.537	6.856	44.230	1.00	21.73	A
ATOM	1407	CD2	HIS	A	184	5.718	7.514	44.147	1.00	20.89	A
ATOM	1408	ND1	HIS	A	184	4.808	5.544	43.914	1.00	18.50	A
ATOM	1409	CE1	HIS	A	184	6.095	5.413	43.649	1.00	20.21	A
ATOM	1410	NE2	HIS	A	184	6.671	6.593	43.784	1.00	20.16	A
ATOM	1411	C	HIS	A	184	3.054	5.802	46.566	1.00	20.29	A
ATOM	1412	O	HIS	A	184	4.095	5.515	47.155	1.00	15.77	A
ATOM	1413	N	HIS	A	185	2.077	4.932	46.326	1.00	19.31	A
ATOM	1414	CA	HIS	A	185	2.123	3.534	46.740	1.00	18.65	A
ATOM	1415	CB	HIS	A	185	3.099	2.755	45.862	1.00	18.24	A
ATOM	1416	CG	HIS	A	185	2.652	2.655	44.437	1.00	22.34	A
ATOM	1417	CD2	HIS	A	185	1.936	1.704	43.793	1.00	21.18	A
ATOM	1418	ND1	HIS	A	185	2.851	3.667	43.523	1.00	20.94	A
ATOM	1419	CE1	HIS	A	185	2.276	3.343	42.378	1.00	24.81	A
ATOM	1420	NE2	HIS	A	185	1.714	2.157	42.516	1.00	21.85	A
ATOM	1421	C	HIS	A	185	2.432	3.309	48.218	1.00	18.84	A
ATOM	1422	O	HIS	A	185	3.068	2.329	48.580	1.00	19.39	A
ATOM	1423	N	ASN	A	186	1.968	4.224	49.063	1.00	16.24	A
ATOM	1424	CA	ASN	A	186	2.170	4.111	50.501	1.00	22.49	A
ATOM	1425	CB	ASN	A	186	2.374	5.490	51.144	1.00	20.05	A
ATOM	1426	CG	ASN	A	186	3.621	6.176	50.665	1.00	18.73	A
ATOM	1427	OD1	ASN	A	186	4.725	5.770	51.000	1.00	19.92	A
ATOM	1428	ND2	ASN	A	186	3.452	7.218	49.863	1.00	19.88	A
ATOM	1429	C	ASN	A	186	.933	3.465	51.125	1.00	23.95	A
ATOM	1430	O	ASN	A	186	-.153	3.486	50.550	1.00	21.53	A
ATOM	1431	N	TRP	A	187	1.121	2.898	52.309	1.00	24.26	A
ATOM	1432	CA	TRP	A	187	.044	2.269	53.058	1.00	24.29	A
ATOM	1433	CB	TRP	A	187	.402	.803	53.342	1.00	22.65	A
ATOM	1434	CG	TRP	A	187	-.637	.026	54.113	1.00	26.54	A
ATOM	1435	CD2	TRP	A	187	-.522	-1.327	54.580	1.00	29.20	A
ATOM	1436	CE2	TRP	A	187	-1.708	-1.630	55.286	1.00	29.59	A
ATOM	1437	CE3	TRP	A	187	.471	-2.309	54.474	1.00	28.24	A

	ATOM	1438	CD1	TRP	A	187	-1.859	.471	54.537	1.00	26.71	A
	ATOM	1439	NE1	TRP	A	187	-2.506	-.519	55.245	1.00	28.42	A
	ATOM	1440	CZ2	TRP	A	187	-1.928	-2.876	55.884	1.00	30.72	A
	ATOM	1441	CZ3	TRP	A	187	.250	-3.550	55.070	1.00	29.93	A
	ATOM	1442	CH2	TRP	A	187	-.941	-3.819	55.766	1.00	29.61	A
	ATOM	1443	C	TRP	A	187	-.117	3.056	54.366	1.00	23.22	A
	ATOM	1444	O	TRP	A	187	.734	2.982	55.257	1.00	25.47	A
	ATOM	1445	N	PHE	A	188	-1.193	3.829	54.464	1.00	23.80	A
	ATOM	1446	CA	PHE	A	188	-1.463	4.622	55.663	1.00	23.83	A
	ATOM	1447	CB	PHE	A	188	-1.919	6.030	55.282	1.00	21.98	A
	ATOM	1448	CG	PHE	A	188	-.918	6.790	54.470	1.00	21.99	A
	ATOM	1449	CD1	PHE	A	188	-1.203	7.162	53.159	1.00	21.36	A
	ATOM	1450	CD2	PHE	A	188	.315	7.127	55.009	1.00	25.03	A
	ATOM	1451	CE1	PHE	A	188	-.271	7.858	52.403	1.00	22.76	A
	ATOM	1452	CE2	PHE	A	188	1.253	7.822	54.258	1.00	26.38	A
	ATOM	1453	CZ	PHE	A	188	.960	8.188	52.953	1.00	24.25	A
	ATOM	1454	C	PHE	A	188	-2.574	3.931	56.441	1.00	24.18	A
	ATOM	1455	O	PHE	A	188	-3.654	3.707	55.901	1.00	25.28	A
	ATOM	1456	N	GLU	A	189	-2.325	3.612	57.707	1.00	22.09	A
	ATOM	1457	CA	GLU	A	189	-3.335	2.912	58.487	1.00	26.71	A
	ATOM	1458	CB	GLU	A	189	-3.131	1.404	58.324	1.00	24.90	A
	ATOM	1459	CG	GLU	A	189	-4.238	.558	58.913	1.00	34.09	A
	ATOM	1460	CD	GLU	A	189	-4.134	-.894	58.486	1.00	37.92	A
	ATOM	1461	OE1	GLU	A	189	-3.401	-1.675	59.141	1.00	37.11	A
	ATOM	1462	OE2	GLU	A	189	-4.776	-1.240	57.477	1.00	39.20	A
	ATOM	1463	C	GLU	A	189	-3.392	3.258	59.971	1.00	23.49	A
	ATOM	1464	O	GLU	A	189	-2.371	3.332	60.637	1.00	24.56	A
	ATOM	1465	N	ASN	A	190	-4.607	3.453	60.472	1.00	26.82	A
	ATOM	1466	CA	ASN	A	190	-4.833	3.768	61.880	1.00	29.45	A
	ATOM	1467	CB	ASN	A	190	-4.397	2.585	62.752	1.00	28.61	A
	ATOM	1468	CG	ASN	A	190	-5.268	2.421	63.977	1.00	41.18	A
	ATOM	1469	OD1	ASN	A	190	-6.490	2.312	63.871	1.00	46.11	A
	ATOM	1470	ND2	ASN	A	190	-4.648	2.404	65.149	1.00	44.12	A
	ATOM	1471	C	ASN	A	190	-4.077	5.027	62.279	1.00	29.39	A
	ATOM	1472	O	ASN	A	190	-3.168	4.994	63.106	1.00	31.76	A
	ATOM	1473	N	LEU	A	191	-4.457	6.139	61.661	1.00	29.54	A
	ATOM	1474	CA	LEU	A	191	-3.828	7.420	61.924	1.00	29.05	A
	ATOM	1475	CB	LEU	A	191	-3.040	7.881	60.693	1.00	29.69	A
	ATOM	1476	CG	LEU	A	191	-1.888	6.994	60.204	1.00	26.98	A
	ATOM	1477	CD1	LEU	A	191	-1.394	7.488	58.854	1.00	25.66	A
	ATOM	1478	CD2	LEU	A	191	-.758	7.002	61.218	1.00	25.53	A
	ATOM	1479	C	LEU	A	191	-4.950	8.392	62.221	1.00	30.01	A
	ATOM	1480	O	LEU	A	191	-5.998	8.352	61.574	1.00	31.64	A
	ATOM	1481	N	ASN	A	192	-4.740	9.266	63.197	1.00	28.63	A
	ATOM	1482	CA	ASN	A	192	-5.777	10.216	63.555	1.00	25.24	A
	ATOM	1483	CB	ASN	A	192	-5.518	10.783	64.945	1.00	29.60	A
	ATOM	1484	CG	ASN	A	192	-6.705	11.537	65.479	1.00	32.33	A
	ATOM	1485	OD1	ASN	A	192	-7.683	10.937	65.919	1.00	37.35	A
	ATOM	1486	ND2	ASN	A	192	-6.644	12.858	65.420	1.00	29.99	A
	ATOM	1487	C	ASN	A	192	-5.937	11.364	62.557	1.00	26.07	A
	ATOM	1488	O	ASN	A	192	-7.028	11.583	62.031	1.00	27.69	A
	ATOM	1489	N	SER	A	193	-4.859	12.100	62.296	1.00	26.71	A
	ATOM	1490	CA	SER	A	193	-4.927	13.223	61.359	1.00	27.54	A
	ATOM	1491	CB	SER	A	193	-5.432	14.475	62.070	1.00	24.51	A
	ATOM	1492	OG	SER	A	193	-4.524	14.845	63.087	1.00	31.94	A
	ATOM	1493	C	SER	A	193	-3.573	13.522	60.726	1.00	25.67	A
	ATOM	1494	O	SER	A	193	-2.574	12.866	61.040	1.00	26.65	A
	ATOM	1495	N	ARG	A	194	-3.556	14.525	59.844	1.00	23.86	A
	ATOM	1496	CA	ARG	A	194	-2.348	14.936	59.126	1.00	24.27	A
	ATOM	1497	CB	ARG	A	194	-1.221	15.279	60.105	1.00	28.68	A
	ATOM	1498	CG	ARG	A	194	-1.516	16.392	61.086	1.00	29.96	A
	ATOM	1499	CD	ARG	A	194	-.265	16.650	61.903	1.00	32.03	A
	ATOM	1500	NE	ARG	A	194	-.425	17.738	62.855	1.00	34.25	A
	ATOM	1501	CZ	ARG	A	194	.535	18.145	63.679	1.00	37.34	A
	ATOM	1502	NH1	ARG	A	194	1.727	17.551	63.667	1.00	32.52	A
	ATOM	1503	NH2	ARG	A	194	.301	19.147	64.513	1.00	34.77	A
	ATOM	1504	C	ARG	A	194	-1.869	13.804	58.225	1.00	17.11	A
	ATOM	1505	O	ARG	A	194	-.798	13.249	58.451	1.00	22.22	A
	ATOM	1506	N	VAL	A	195	-2.643	13.469	57.197	1.00	23.35	A

ATOM	1507	CA	VAL	A	195	-2.259	12.366	56.323	1.00	21.08	A
ATOM	1508	CB	VAL	A	195	-3.234	11.165	56.514	1.00	21.28	A
ATOM	1509	CG1	VAL	A	195	-2.582	9.856	56.052	1.00	22.15	A
ATOM	1510	CG2	VAL	A	195	-3.649	11.069	57.972	1.00	20.62	A
ATOM	1511	C	VAL	A	195	-2.194	12.754	54.843	1.00	22.50	A
ATOM	1512	O	VAL	A	195	-2.819	12.119	53.993	1.00	19.95	A
ATOM	1513	N	PRO	A	196	-1.426	13.804	54.516	1.00	22.21	A
ATOM	1514	CD	PRO	A	196	-.966	14.003	53.127	1.00	23.62	A
ATOM	1515	CA	PRO	A	196	-.634	14.634	55.428	1.00	22.20	A
ATOM	1516	CB	PRO	A	196	.700	14.697	54.718	1.00	26.49	A
ATOM	1517	CG	PRO	A	196	.243	14.938	53.294	1.00	26.84	A
ATOM	1518	C	PRO	A	196	-1.240	16.032	55.541	1.00	23.00	A
ATOM	1519	O	PRO	A	196	-2.173	16.366	54.812	1.00	19.52	A
ATOM	1520	N	SER	A	197	-.709	16.833	56.461	1.00	21.62	A
ATOM	1521	CA	SER	A	197	-1.129	18.221	56.603	1.00	24.42	A
ATOM	1522	CB	SER	A	197	-.915	18.727	58.029	1.00	25.20	A
ATOM	1523	OG	SER	A	197	-1.191	20.114	58.108	1.00	25.92	A
ATOM	1524	C	SER	A	197	-.147	18.902	55.648	1.00	23.29	A
ATOM	1525	O	SER	A	197	1.071	18.786	55.817	1.00	23.28	A
ATOM	1526	N	PHE	A	198	-.674	19.603	54.649	1.00	24.07	A
ATOM	1527	CA	PHE	A	198	.162	20.220	53.622	1.00	23.25	A
ATOM	1528	CB	PHE	A	198	-.141	19.498	52.300	1.00	26.64	A
ATOM	1529	CG	PHE	A	198	1.007	19.445	51.332	1.00	24.18	A
ATOM	1530	CD1	PHE	A	198	1.306	20.532	50.517	1.00	25.20	A
ATOM	1531	CD2	PHE	A	198	1.762	18.287	51.202	1.00	26.18	A
ATOM	1532	CE1	PHE	A	198	2.335	20.468	49.583	1.00	23.60	A
ATOM	1533	CE2	PHE	A	198	2.796	18.209	50.271	1.00	28.79	A
ATOM	1534	CZ	PHE	A	198	3.081	19.307	49.458	1.00	28.17	A
ATOM	1535	C	PHE	A	198	-.038	21.737	53.469	1.00	23.34	A
ATOM	1536	O	PHE	A	198	-1.047	22.184	52.928	1.00	23.70	A
ATOM	1537	N	ARG	A	199	.936	22.512	53.949	1.00	24.58	A
ATOM	1538	CA	ARG	A	199	.912	23.974	53.871	1.00	19.79	A
ATOM	1539	CB	ARG	A	199	1.428	24.594	55.172	1.00	22.90	A
ATOM	1540	CG	ARG	A	199	.553	24.445	56.402	1.00	23.00	A
ATOM	1541	CD	ARG	A	199	1.249	25.122	57.575	1.00	26.82	A
ATOM	1542	NE	ARG	A	199	.360	25.403	58.700	1.00	26.21	A
ATOM	1543	CZ	ARG	A	199	.416	24.765	59.863	1.00	30.21	A
ATOM	1544	NH1	ARG	A	199	1.316	23.810	60.045	1.00	27.07	A
ATOM	1545	NH2	ARG	A	199	-.408	25.095	60.847	1.00	29.65	A
ATOM	1546	C	ARG	A	199	1.815	24.453	52.734	1.00	20.00	A
ATOM	1547	O	ARG	A	199	2.989	24.092	52.685	1.00	22.25	A
ATOM	1548	N	PHE	A	200	1.272	25.273	51.835	1.00	22.47	A
ATOM	1549	CA	PHE	A	200	2.030	25.805	50.700	1.00	25.47	A
ATOM	1550	CB	PHE	A	200	3.231	26.644	51.173	1.00	25.51	A
ATOM	1551	CG	PHE	A	200	2.888	27.740	52.154	1.00	27.55	A
ATOM	1552	CD1	PHE	A	200	2.917	27.500	53.524	1.00	25.03	A
ATOM	1553	CD2	PHE	A	200	2.588	29.022	51.709	1.00	29.74	A
ATOM	1554	CE1	PHE	A	200	2.658	28.527	54.441	1.00	26.41	A
ATOM	1555	CE2	PHE	A	200	2.325	30.057	52.616	1.00	28.45	A
ATOM	1556	CZ	PHE	A	200	2.362	29.807	53.984	1.00	24.13	A
ATOM	1557	C	PHE	A	200	2.577	24.680	49.817	1.00	28.23	A
ATOM	1558	O	PHE	A	200	2.341	23.502	50.076	1.00	25.90	A
ATOM	1559	N	GLY	A	201	3.310	25.058	48.773	1.00	22.42	A
ATOM	1560	CA	GLY	A	201	3.915	24.075	47.890	1.00	20.77	A
ATOM	1561	C	GLY	A	201	3.069	23.334	46.865	1.00	20.82	A
ATOM	1562	O	GLY	A	201	1.905	23.650	46.621	1.00	17.98	A
ATOM	1563	N	GLU	A	202	3.701	22.333	46.256	1.00	19.78	A
ATOM	1564	CA	GLU	A	202	3.084	21.491	45.239	1.00	22.90	A
ATOM	1565	CB	GLU	A	202	3.801	21.648	43.897	1.00	22.56	A
ATOM	1566	CG	GLU	A	202	3.712	23.019	43.276	1.00	29.31	A
ATOM	1567	CD	GLU	A	202	4.715	23.200	42.151	1.00	30.60	A
ATOM	1568	OE1	GLU	A	202	4.886	22.274	41.335	1.00	25.28	A
ATOM	1569	OE2	GLU	A	202	5.337	24.275	42.078	1.00	34.86	A
ATOM	1570	C	GLU	A	202	3.206	20.044	45.676	1.00	20.09	A
ATOM	1571	O	GLU	A	202	4.277	19.600	46.089	1.00	21.63	A
ATOM	1572	N	GLY	A	203	2.113	19.308	45.569	1.00	20.20	A
ATOM	1573	CA	GLY	A	203	2.141	17.915	45.962	1.00	22.92	A
ATOM	1574	C	GLY	A	203	1.457	17.011	44.956	1.00	25.07	A
ATOM	1575	O	GLY	A	203	.702	17.473	44.094	1.00	21.47	A

ATOM	1576	N	HIS	A	204	1.748	15.719	45.065	1.00	19.79	A
ATOM	1577	CA	HIS	A	204	1.162	14.708	44.204	1.00	16.92	A
ATOM	1578	CB	HIS	A	204	2.101	14.369	43.040	1.00	15.22	A
ATOM	1579	CG	HIS	A	204	1.469	13.521	41.976	1.00	17.25	A
ATOM	1580	CD2	HIS	A	204	.181	13.146	41.778	1.00	14.79	A
ATOM	1581	ND1	HIS	A	204	2.187	12.975	40.935	1.00	18.26	A
ATOM	1582	CE1	HIS	A	204	1.372	12.303	40.143	1.00	17.62	A
ATOM	1583	NE2	HIS	A	204	.149	12.391	40.632	1.00	17.84	A
ATOM	1584	C	HIS	A	204	.949	13.483	45.082	1.00	17.79	A
ATOM	1585	O	HIS	A	204	1.904	12.906	45.609	1.00	17.66	A
ATOM	1586	N	ILE	A	205	-.308	13.097	45.248	1.00	15.56	A
ATOM	1587	CA	ILE	A	205	-.649	11.948	46.071	1.00	16.07	A
ATOM	1588	CB	ILE	A	205	-1.514	12.386	47.277	1.00	19.14	A
ATOM	1589	CG2	ILE	A	205	-1.804	11.197	48.181	1.00	19.12	A
ATOM	1590	CG1	ILE	A	205	-.785	13.484	48.058	1.00	18.75	A
ATOM	1591	CD1	ILE	A	205	-1.572	14.048	49.232	1.00	18.52	A
ATOM	1592	C	ILE	A	205	-1.410	10.945	45.214	1.00	18.97	A
ATOM	1593	O	ILE	A	205	-2.563	11.180	44.850	1.00	19.46	A
ATOM	1594	N	TYR	A	206	-.765	9.832	44.878	1.00	19.09	A
ATOM	1595	CA	TYR	A	206	-1.428	8.832	44.039	1.00	19.08	A
ATOM	1596	CB	TYR	A	206	-1.103	9.094	42.560	1.00	19.46	A
ATOM	1597	CG	TYR	A	206	.309	8.763	42.134	1.00	19.31	A
ATOM	1598	CD1	TYR	A	206	.634	7.498	41.643	1.00	20.83	A
ATOM	1599	CE1	TYR	A	206	1.926	7.204	41.194	1.00	18.19	A
ATOM	1600	CD2	TYR	A	206	1.312	9.725	42.173	1.00	18.04	A
ATOM	1601	CE2	TYR	A	206	2.602	9.446	41.729	1.00	18.31	A
ATOM	1602	CZ	TYR	A	206	2.900	8.185	41.239	1.00	22.20	A
ATOM	1603	OH	TYR	A	206	4.170	7.911	40.783	1.00	25.63	A
ATOM	1604	C	TYR	A	206	-1.123	7.376	44.380	1.00	20.31	A
ATOM	1605	O	TYR	A	206	-.085	7.058	44.962	1.00	16.29	A
ATOM	1606	N	ASN	A	207	-2.058	6.507	44.001	1.00	21.83	A
ATOM	1607	CA	ASN	A	207	-1.946	5.074	44.226	1.00	20.84	A
ATOM	1608	CB	ASN	A	207	-.928	4.470	43.250	1.00	16.70	A
ATOM	1609	CG	ASN	A	207	-1.472	4.334	41.822	1.00	21.19	A
ATOM	1610	OD1	ASN	A	207	-.707	4.193	40.871	1.00	19.23	A
ATOM	1611	ND2	ASN	A	207	-2.787	4.359	41.677	1.00	17.72	A
ATOM	1612	C	ASN	A	207	-1.564	4.721	45.667	1.00	18.26	A
ATOM	1613	O	ASN	A	207	-.753	3.826	45.892	1.00	23.53	A
ATOM	1614	N	ASN	A	208	-2.138	5.434	46.632	1.00	19.34	A
ATOM	1615	CA	ASN	A	208	-1.885	5.165	48.047	1.00	19.45	A
ATOM	1616	CB	ASN	A	208	-1.672	6.460	48.843	1.00	20.00	A
ATOM	1617	CG	ASN	A	208	-.456	7.237	48.394	1.00	20.98	A
ATOM	1618	OD1	ASN	A	208	.682	6.847	48.662	1.00	22.40	A
ATOM	1619	ND2	ASN	A	208	-.692	8.340	47.700	1.00	19.20	A
ATOM	1620	C	ASN	A	208	-3.116	4.469	48.610	1.00	23.47	A
ATOM	1621	O	ASN	A	208	-4.221	4.616	48.082	1.00	21.55	A
ATOM	1622	N	TYR	A	209	-2.924	3.716	49.686	1.00	22.42	A
ATOM	1623	CA	TYR	A	209	-4.028	3.026	50.334	1.00	23.96	A
ATOM	1624	CB	TYR	A	209	-3.748	1.520	50.394	1.00	23.00	A
ATOM	1625	CG	TYR	A	209	-4.721	.737	51.248	1.00	23.28	A
ATOM	1626	CD1	TYR	A	209	-6.090	.912	51.114	1.00	27.75	A
ATOM	1627	CE1	TYR	A	209	-6.986	.190	51.887	1.00	34.06	A
ATOM	1628	CD2	TYR	A	209	-4.263	-.191	52.180	1.00	27.63	A
ATOM	1629	CE2	TYR	A	209	-5.148	-.930	52.963	1.00	26.68	A
ATOM	1630	CZ	TYR	A	209	-6.507	-.731	52.815	1.00	33.00	A
ATOM	1631	OH	TYR	A	209	-7.392	-1.431	53.602	1.00	39.00	A
ATOM	1632	C	TYR	A	209	-4.208	3.596	51.742	1.00	21.89	A
ATOM	1633	O	TYR	A	209	-3.309	3.501	52.576	1.00	22.58	A
ATOM	1634	N	PHE	A	210	-5.360	4.218	51.985	1.00	23.25	A
ATOM	1635	CA	PHE	A	210	-5.659	4.801	53.292	1.00	23.43	A
ATOM	1636	CB	PHE	A	210	-6.240	6.217	53.170	1.00	23.68	A
ATOM	1637	CG	PHE	A	210	-5.329	7.221	52.519	1.00	25.54	A
ATOM	1638	CD1	PHE	A	210	-5.134	7.214	51.144	1.00	23.54	A
ATOM	1639	CD2	PHE	A	210	-4.717	8.216	53.279	1.00	25.45	A
ATOM	1640	CE1	PHE	A	210	-4.350	8.184	50.532	1.00	23.31	A
ATOM	1641	CE2	PHE	A	210	-3.930	9.192	52.678	1.00	25.27	A
ATOM	1642	CZ	PHE	A	210	-3.748	9.175	51.303	1.00	26.92	A
ATOM	1643	C	PHE	A	210	-6.704	3.950	53.998	1.00	24.47	A
ATOM	1644	O	PHE	A	210	-7.781	3.716	53.454	1.00	26.37	A

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ATOM   1645  N   ASN A 211      -6.405   3.507  55.210  1.00 23.37      A
ATOM   1646  CA  ASN A 211      -7.366   2.701  55.955  1.00 25.63      A
ATOM   1647  CB  ASN A 211      -7.012   1.216  55.857  1.00 24.24      A
ATOM   1648  CG  ASN A 211      -8.006    .329  56.601  1.00 27.65      A
ATOM   1649  OD1 ASN A 211      -9.216    .469  56.445  1.00 28.51      A
ATOM   1650  ND2 ASN A 211      -7.492   -.591  57.403  1.00 26.94      A
ATOM   1651  C   ASN A 211      -7.422   3.133  57.416  1.00 21.84      A
ATOM   1652  O   ASN A 211      -6.393   3.283  58.074  1.00 21.94      A
ATOM   1653  N   LYS A 212      -8.639   3.338  57.905  1.00 24.84      A
ATOM   1654  CA  LYS A 212      -8.863   3.770  59.279  1.00 26.83      A
ATOM   1655  CB  LYS A 212      -8.349   2.715  60.260  1.00 25.58      A
ATOM   1656  CG  LYS A 212      -9.061   1.379  60.121  1.00 36.55      A
ATOM   1657  CD  LYS A 212      -9.286    .703  61.461  1.00 49.30      A
ATOM   1658  CE  LYS A 212      -7.980    .344  62.144  1.00 53.55      A
ATOM   1659  NZ  LYS A 212      -8.219   -.384  63.434  1.00 60.03      A
ATOM   1660  C   LYS A 212      -8.239   5.133  59.597  1.00 28.04      A
ATOM   1661  O   LYS A 212      -7.308   5.241  60.395  1.00 26.12      A
ATOM   1662  N   ILE A 213      -8.745   6.167  58.936  1.00 29.69      A
ATOM   1663  CA  ILE A 213      -8.283   7.526  59.180  1.00 29.17      A
ATOM   1664  CB  ILE A 213      -8.295   8.366  57.891  1.00 28.23      A
ATOM   1665  CG2 ILE A 213      -7.689   9.730  58.156  1.00 27.71      A
ATOM   1666  CG1 ILE A 213      -7.514   7.633  56.797  1.00 30.52      A
ATOM   1667  CD1 ILE A 213      -6.093   7.258  57.180  1.00 28.90      A
ATOM   1668  C   ILE A 213      -9.336   8.020  60.161  1.00 28.41      A
ATOM   1669  O   ILE A 213     -10.491   8.241  59.795  1.00 24.32      A
ATOM   1670  N   ILE A 214      -8.925   8.157  61.414  1.00 28.32      A
ATOM   1671  CA  ILE A 214      -9.820   8.544  62.497  1.00 29.16      A
ATOM   1672  CB  ILE A 214      -9.110   8.413  63.860  1.00 31.74      A
ATOM   1673  CG2 ILE A 214     -10.149   8.344  64.980  1.00 31.23      A
ATOM   1674  CG1 ILE A 214      -8.243   7.154  63.885  1.00 33.15      A
ATOM   1675  CD1 ILE A 214      -8.961   5.900  63.447  1.00 35.01      A
ATOM   1676  C   ILE A 214     -10.493   9.912  62.450  1.00 27.00      A
ATOM   1677  O   ILE A 214     -11.715   9.991  62.507  1.00 29.50      A
ATOM   1678  N   ASP A 215      -9.722  10.990  62.358  1.00 28.06      A
ATOM   1679  CA  ASP A 215     -10.336  12.312  62.350  1.00 23.94      A
ATOM   1680  CB  ASP A 215      -9.682  13.188  63.415  1.00 28.45      A
ATOM   1681  CG  ASP A 215     -10.525  14.401  63.756  1.00 35.85      A
ATOM   1682  OD1 ASP A 215     -11.750  14.236  63.935  1.00 39.14      A
ATOM   1683  OD2 ASP A 215      -9.972  15.514  63.844  1.00 39.83      A
ATOM   1684  C   ASP A 215     -10.333  13.024  60.998  1.00 26.59      A
ATOM   1685  O   ASP A 215     -11.342  13.592  60.593  1.00 26.86      A
ATOM   1686  N   SER A 216      -9.204  12.997  60.299  1.00 26.57      A
ATOM   1687  CA  SER A 216      -9.109  13.624  58.987  1.00 22.27      A
ATOM   1688  CB  SER A 216      -9.122  15.153  59.116  1.00 24.64      A
ATOM   1689  OG  SER A 216      -8.025  15.614  59.874  1.00 25.08      A
ATOM   1690  C   SER A 216      -7.837  13.159  58.287  1.00 23.71      A
ATOM   1691  O   SER A 216      -6.840  12.831  58.936  1.00 20.77      A
ATOM   1692  N   GLY A 217      -7.875  13.132  56.961  1.00 22.80      A
ATOM   1693  CA  GLY A 217      -6.719  12.681  56.211  1.00 23.77      A
ATOM   1694  C   GLY A 217      -5.882  13.773  55.571  1.00 21.52      A
ATOM   1695  O   GLY A 217      -5.114  14.455  56.247  1.00 20.73      A
ATOM   1696  N   ILE A 218      -6.027  13.927  54.260  1.00 20.64      A
ATOM   1697  CA  ILE A 218      -5.277  14.927  53.515  1.00 19.50      A
ATOM   1698  CB  ILE A 218      -5.369  14.674  52.008  1.00 17.48      A
ATOM   1699  CG2 ILE A 218      -4.500  15.672  51.258  1.00 18.81      A
ATOM   1700  CG1 ILE A 218      -4.929  13.246  51.690  1.00 19.30      A
ATOM   1701  CD1 ILE A 218      -5.189  12.851  50.257  1.00 22.16      A
ATOM   1702  C   ILE A 218      -5.814  16.325  53.798  1.00 20.32      A
ATOM   1703  O   ILE A 218      -6.973  16.620  53.522  1.00 21.51      A
ATOM   1704  N   ASN A 219      -4.968  17.182  54.351  1.00 22.47      A
ATOM   1705  CA  ASN A 219      -5.374  18.544  54.656  1.00 21.92      A
ATOM   1706  CB  ASN A 219      -5.225  18.831  56.156  1.00 20.26      A
ATOM   1707  CG  ASN A 219      -5.784  20.185  56.549  1.00 22.01      A
ATOM   1708  OD1 ASN A 219      -6.430  20.862  55.747  1.00 18.67      A
ATOM   1709  ND2 ASN A 219      -5.543  20.584  57.788  1.00 22.12      A
ATOM   1710  C   ASN A 219      -4.528  19.516  53.840  1.00 23.49      A
ATOM   1711  O   ASN A 219      -3.373  19.792  54.169  1.00 20.73      A
ATOM   1712  N   SER A 220      -5.112  20.012  52.757  1.00 17.83      A
ATOM   1713  CA  SER A 220      -4.430  20.949  51.892  1.00 21.44      A
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ATOM	1714	CB	SER	A	220	-4.973	20.841	50.472	1.00	18.06	A
ATOM	1715	OG	SER	A	220	-4.261	21.684	49.593	1.00	20.00	A
ATOM	1716	C	SER	A	220	-4.665	22.351	52.440	1.00	22.92	A
ATOM	1717	O	SER	A	220	-5.804	22.746	52.682	1.00	23.16	A
ATOM	1718	N	ARG	A	221	-3.592	23.105	52.634	1.00	24.19	A
ATOM	1719	CA	ARG	A	221	-3.738	24.449	53.178	1.00	26.19	A
ATOM	1720	CB	ARG	A	221	-3.796	24.377	54.710	1.00	29.78	A
ATOM	1721	CG	ARG	A	221	-2.798	23.426	55.332	1.00	30.44	A
ATOM	1722	CD	ARG	A	221	-3.272	22.713	56.611	1.00	25.72	A
ATOM	1723	NE	ARG	A	221	-3.177	23.470	57.814	1.00	23.61	A
ATOM	1724	CZ	ARG	A	221	-2.884	23.139	59.069	1.00	29.45	A
ATOM	1725	NH1	ARG	A	221	-2.941	24.155	59.905	1.00	28.93	A
ATOM	1726	NH2	ARG	A	221	-2.529	21.936	59.519	1.00	23.01	A
ATOM	1727	C	ARG	A	221	-2.717	25.493	52.745	1.00	25.85	A
ATOM	1728	O	ARG	A	221	-1.685	25.188	52.145	1.00	21.79	A
ATOM	1729	N	MET	A	222	-3.045	26.742	53.056	1.00	23.33	A
ATOM	1730	CA	MET	A	222	-2.204	27.887	52.727	1.00	22.37	A
ATOM	1731	CB	MET	A	222	-.977	27.912	53.642	1.00	19.79	A
ATOM	1732	CG	MET	A	222	-1.325	28.143	55.120	1.00	22.92	A
ATOM	1733	SD	MET	A	222	-2.231	29.699	55.409	1.00	25.93	A
ATOM	1734	CE	MET	A	222	-.893	30.882	55.158	1.00	26.81	A
ATOM	1735	C	MET	A	222	-1.783	27.936	51.255	1.00	20.65	A
ATOM	1736	O	MET	A	222	-.611	28.085	50.938	1.00	18.70	A
ATOM	1737	N	GLY	A	223	-2.759	27.794	50.366	1.00	19.69	A
ATOM	1738	CA	GLY	A	223	-2.489	27.865	48.941	1.00	22.92	A
ATOM	1739	C	GLY	A	223	-1.792	26.679	48.298	1.00	24.13	A
ATOM	1740	O	GLY	A	223	-1.315	26.781	47.166	1.00	22.09	A
ATOM	1741	N	ALA	A	224	-1.727	25.556	49.000	1.00	17.68	A
ATOM	1742	CA	ALA	A	224	-1.087	24.375	48.441	1.00	18.58	A
ATOM	1743	CB	ALA	A	224	-.993	23.272	49.501	1.00	20.14	A
ATOM	1744	C	ALA	A	224	-1.882	23.872	47.229	1.00	19.67	A
ATOM	1745	O	ALA	A	224	-3.107	23.984	47.186	1.00	18.44	A
ATOM	1746	N	ARG	A	225	-1.170	23.357	46.234	1.00	17.63	A
ATOM	1747	CA	ARG	A	225	-1.808	22.796	45.046	1.00	22.58	A
ATOM	1748	CB	ARG	A	225	-1.326	23.512	43.786	1.00	22.92	A
ATOM	1749	CG	ARG	A	225	-1.850	24.941	43.647	1.00	25.13	A
ATOM	1750	CD	ARG	A	225	-1.113	25.682	42.533	1.00	32.38	A
ATOM	1751	NE	ARG	A	225	.304	25.813	42.847	1.00	32.69	A
ATOM	1752	CZ	ARG	A	225	1.283	25.758	41.949	1.00	38.83	A
ATOM	1753	NH1	ARG	A	225	2.545	25.893	42.345	1.00	40.85	A
ATOM	1754	NH2	ARG	A	225	1.008	25.567	40.663	1.00	30.17	A
ATOM	1755	C	ARG	A	225	-1.422	21.319	45.019	1.00	21.45	A
ATOM	1756	O	ARG	A	225	-.256	20.972	44.819	1.00	21.15	A
ATOM	1757	N	ILE	A	226	-2.401	20.454	45.252	1.00	19.50	A
ATOM	1758	CA	ILE	A	226	-2.144	19.026	45.298	1.00	20.77	A
ATOM	1759	CB	ILE	A	226	-2.406	18.459	46.706	1.00	17.00	A
ATOM	1760	CG2	ILE	A	226	-1.906	17.029	46.782	1.00	18.12	A
ATOM	1761	CG1	ILE	A	226	-1.722	19.331	47.759	1.00	19.81	A
ATOM	1762	CD1	ILE	A	226	-1.943	18.856	49.184	1.00	23.76	A
ATOM	1763	C	ILE	A	226	-2.976	18.213	44.322	1.00	22.65	A
ATOM	1764	O	ILE	A	226	-4.200	18.324	44.281	1.00	22.92	A
ATOM	1765	N	ARG	A	227	-2.289	17.390	43.541	1.00	21.22	A
ATOM	1766	CA	ARG	A	227	-2.933	16.505	42.585	1.00	19.03	A
ATOM	1767	CB	ARG	A	227	-1.995	16.263	41.403	1.00	22.63	A
ATOM	1768	CG	ARG	A	227	-2.499	15.295	40.369	1.00	25.97	A
ATOM	1769	CD	ARG	A	227	-3.674	15.852	39.606	1.00	28.32	A
ATOM	1770	NE	ARG	A	227	-3.974	14.979	38.487	1.00	39.21	A
ATOM	1771	CZ	ARG	A	227	-3.738	15.269	37.214	1.00	33.81	A
ATOM	1772	NH1	ARG	A	227	-3.206	16.431	36.879	1.00	32.29	A
ATOM	1773	NH2	ARG	A	227	-4.018	14.372	36.279	1.00	35.47	A
ATOM	1774	C	ARG	A	227	-3.158	15.213	43.371	1.00	17.99	A
ATOM	1775	O	ARG	A	227	-2.201	14.586	43.822	1.00	18.38	A
ATOM	1776	N	ILE	A	228	-4.417	14.831	43.545	1.00	17.92	A
ATOM	1777	CA	ILE	A	228	-4.768	13.626	44.302	1.00	18.43	A
ATOM	1778	CB	ILE	A	228	-5.622	13.997	45.530	1.00	20.12	A
ATOM	1779	CG2	ILE	A	228	-5.804	12.776	46.428	1.00	19.24	A
ATOM	1780	CG1	ILE	A	228	-4.948	15.142	46.299	1.00	21.74	A
ATOM	1781	CD1	ILE	A	228	-5.848	15.824	47.316	1.00	21.21	A
ATOM	1782	C	ILE	A	228	-5.566	12.678	43.407	1.00	21.20	A

ATOM	1783	O	ILE	A	228	-6.723	12.947	43.088	1.00	21.54	A
ATOM	1784	N	GLU	A	229	-4.964	11.563	43.018	1.00	17.62	A
ATOM	1785	CA	GLU	A	229	-5.651	10.652	42.114	1.00	22.42	A
ATOM	1786	CB	GLU	A	229	-5.281	11.036	40.673	1.00	24.37	A
ATOM	1787	CG	GLU	A	229	-3.834	10.726	40.304	1.00	26.99	A
ATOM	1788	CD	GLU	A	229	-3.286	11.600	39.185	1.00	22.81	A
ATOM	1789	OE1	GLU	A	229	-4.064	12.039	38.322	1.00	23.87	A
ATOM	1790	OE2	GLU	A	229	-2.067	11.839	39.165	1.00	19.72	A
ATOM	1791	C	GLU	A	229	-5.400	9.151	42.338	1.00	21.08	A
ATOM	1792	O	GLU	A	229	-4.363	8.745	42.863	1.00	19.85	A
ATOM	1793	N	ASN	A	230	-6.380	8.341	41.947	1.00	23.01	A
ATOM	1794	CA	ASN	A	230	-6.286	6.890	42.051	1.00	20.20	A
ATOM	1795	CB	ASN	A	230	-5.332	6.360	40.976	1.00	16.89	A
ATOM	1796	CG	ASN	A	230	-5.880	6.530	39.568	1.00	25.22	A
ATOM	1797	OD1	ASN	A	230	-6.420	7.585	39.217	1.00	26.28	A
ATOM	1798	ND2	ASN	A	230	-5.734	5.489	38.747	1.00	26.56	A
ATOM	1799	C	ASN	A	230	-5.849	6.378	43.424	1.00	20.33	A
ATOM	1800	O	ASN	A	230	-5.009	5.479	43.528	1.00	23.53	A
ATOM	1801	N	ASN	A	231	-6.415	6.963	44.471	1.00	18.23	A
ATOM	1802	CA	ASN	A	231	-6.120	6.544	45.837	1.00	20.81	A
ATOM	1803	CB	ASN	A	231	-5.907	7.750	46.761	1.00	17.70	A
ATOM	1804	CG	ASN	A	231	-4.666	8.538	46.427	1.00	19.25	A
ATOM	1805	OD1	ASN	A	231	-3.548	8.107	46.704	1.00	16.94	A
ATOM	1806	ND2	ASN	A	231	-4.858	9.703	45.818	1.00	17.58	A
ATOM	1807	C	ASN	A	231	-7.343	5.788	46.338	1.00	22.87	A
ATOM	1808	O	ASN	A	231	-8.451	6.036	45.876	1.00	24.26	A
ATOM	1809	N	LEU	A	232	-7.143	4.872	47.278	1.00	21.95	A
ATOM	1810	CA	LEU	A	232	-8.260	4.140	47.856	1.00	25.72	A
ATOM	1811	CB	LEU	A	232	-8.075	2.622	47.725	1.00	28.58	A
ATOM	1812	CG	LEU	A	232	-9.120	1.848	48.550	1.00	33.77	A
ATOM	1813	CD1	LEU	A	232	-10.500	2.094	47.977	1.00	30.45	A
ATOM	1814	CD2	LEU	A	232	-8.801	.361	48.553	1.00	33.21	A
ATOM	1815	C	LEU	A	232	-8.360	4.497	49.332	1.00	22.86	A
ATOM	1816	O	LEU	A	232	-7.390	4.344	50.082	1.00	23.72	A
ATOM	1817	N	PHE	A	233	-9.527	4.985	49.744	1.00	23.90	A
ATOM	1818	CA	PHE	A	233	-9.755	5.345	51.144	1.00	25.59	A
ATOM	1819	CB	PHE	A	233	-10.310	6.773	51.287	1.00	26.06	A
ATOM	1820	CG	PHE	A	233	-9.440	7.848	50.695	1.00	25.69	A
ATOM	1821	CD1	PHE	A	233	-9.521	8.166	49.346	1.00	21.43	A
ATOM	1822	CD2	PHE	A	233	-8.560	8.563	51.496	1.00	26.42	A
ATOM	1823	CE1	PHE	A	233	-8.736	9.187	48.802	1.00	24.88	A
ATOM	1824	CE2	PHE	A	233	-7.771	9.583	50.962	1.00	25.84	A
ATOM	1825	CZ	PHE	A	233	-7.863	9.894	49.612	1.00	23.17	A
ATOM	1826	C	PHE	A	233	-10.785	4.386	51.740	1.00	26.90	A
ATOM	1827	O	PHE	A	233	-11.902	4.270	51.233	1.00	28.21	A
ATOM	1828	N	GLU	A	234	-10.410	3.696	52.806	1.00	26.34	A
ATOM	1829	CA	GLU	A	234	-11.327	2.780	53.478	1.00	31.73	A
ATOM	1830	CB	GLU	A	234	-10.806	1.339	53.434	1.00	36.57	A
ATOM	1831	CG	GLU	A	234	-11.103	.596	52.151	1.00	44.30	A
ATOM	1832	CD	GLU	A	234	-10.628	-.856	52.191	1.00	44.61	A
ATOM	1833	OE1	GLU	A	234	-10.875	-1.569	51.194	1.00	50.77	A
ATOM	1834	OE2	GLU	A	234	-10.012	-1.282	53.200	1.00	41.13	A
ATOM	1835	C	GLU	A	234	-11.458	3.191	54.932	1.00	26.89	A
ATOM	1836	O	GLU	A	234	-10.460	3.494	55.575	1.00	29.08	A
ATOM	1837	N	ASN	A	235	-12.685	3.181	55.443	1.00	28.60	A
ATOM	1838	CA	ASN	A	235	-12.942	3.537	56.835	1.00	30.55	A
ATOM	1839	CB	ASN	A	235	-12.418	2.438	57.773	1.00	32.66	A
ATOM	1840	CG	ASN	A	235	-12.932	1.053	57.397	1.00	40.61	A
ATOM	1841	OD1	ASN	A	235	-14.133	.861	57.209	1.00	44.95	A
ATOM	1842	ND2	ASN	A	235	-12.025	.081	57.291	1.00	36.48	A
ATOM	1843	C	ASN	A	235	-12.243	4.850	57.149	1.00	26.93	A
ATOM	1844	O	ASN	A	235	-11.427	4.929	58.061	1.00	24.98	A
ATOM	1845	N	ALA	A	236	-12.561	5.878	56.373	1.00	29.55	A
ATOM	1846	CA	ALA	A	236	-11.944	7.177	56.561	1.00	30.18	A
ATOM	1847	CB	ALA	A	236	-11.094	7.531	55.339	1.00	29.05	A
ATOM	1848	C	ALA	A	236	-12.958	8.274	56.809	1.00	27.65	A
ATOM	1849	O	ALA	A	236	-14.012	8.317	56.178	1.00	31.17	A
ATOM	1850	N	LYS	A	237	-12.623	9.161	57.738	1.00	29.77	A
ATOM	1851	CA	LYS	A	237	-13.467	10.299	58.063	1.00	28.35	A

ATOM	1852	CB	LYS	A	237	-13.647	10.416	59.576	1.00	29.79	A
ATOM	1853	CG	LYS	A	237	-14.333	11.703	60.009	1.00	31.96	A
ATOM	1854	CD	LYS	A	237	-14.465	11.782	61.512	1.00	35.37	A
ATOM	1855	CE	LYS	A	237	-14.910	13.168	61.928	1.00	33.16	A
ATOM	1856	NZ	LYS	A	237	-13.957	14.206	61.455	1.00	29.06	A
ATOM	1857	C	LYS	A	237	-12.769	11.551	57.534	1.00	29.10	A
ATOM	1858	O	LYS	A	237	-11.604	11.790	57.845	1.00	27.41	A
ATOM	1859	N	ASP	A	238	-13.476	12.336	56.732	1.00	27.06	A
ATOM	1860	CA	ASP	A	238	-12.910	13.555	56.171	1.00	27.75	A
ATOM	1861	CB	ASP	A	238	-12.798	14.614	57.277	1.00	26.88	A
ATOM	1862	CG	ASP	A	238	-14.157	15.070	57.782	1.00	29.98	A
ATOM	1863	OD1	ASP	A	238	-14.938	15.608	56.968	1.00	29.32	A
ATOM	1864	OD2	ASP	A	238	-14.446	14.880	58.982	1.00	28.61	A
ATOM	1865	C	ASP	A	238	-11.540	13.284	55.535	1.00	27.54	A
ATOM	1866	O	ASP	A	238	-10.524	13.852	55.942	1.00	30.61	A
ATOM	1867	N	PRO	A	239	-11.503	12.402	54.523	1.00	27.59	A
ATOM	1868	CD	PRO	A	239	-12.643	11.652	53.967	1.00	27.53	A
ATOM	1869	CA	PRO	A	239	-10.255	12.050	53.835	1.00	25.34	A
ATOM	1870	CB	PRO	A	239	-10.680	10.900	52.915	1.00	26.26	A
ATOM	1871	CG	PRO	A	239	-12.118	11.222	52.613	1.00	30.67	A
ATOM	1872	C	PRO	A	239	-9.569	13.195	53.091	1.00	19.57	A
ATOM	1873	O	PRO	A	239	-8.362	13.180	52.914	1.00	20.57	A
ATOM	1874	N	ILE	A	240	-10.338	14.188	52.661	1.00	22.19	A
ATOM	1875	CA	ILE	A	240	-9.766	15.330	51.960	1.00	22.54	A
ATOM	1876	CB	ILE	A	240	-9.956	15.214	50.436	1.00	24.29	A
ATOM	1877	CG2	ILE	A	240	-9.340	16.423	49.737	1.00	25.22	A
ATOM	1878	CG1	ILE	A	240	-9.302	13.926	49.923	1.00	22.98	A
ATOM	1879	CD1	ILE	A	240	-9.543	13.686	48.450	1.00	26.19	A
ATOM	1880	C	ILE	A	240	-10.427	16.621	52.435	1.00	22.16	A
ATOM	1881	O	ILE	A	240	-11.623	16.832	52.216	1.00	21.64	A
ATOM	1882	N	VAL	A	241	-9.645	17.483	53.080	1.00	20.41	A
ATOM	1883	CA	VAL	A	241	-10.173	18.749	53.587	1.00	24.90	A
ATOM	1884	CB	VAL	A	241	-10.552	18.646	55.093	1.00	23.21	A
ATOM	1885	CG1	VAL	A	241	-11.618	17.595	55.310	1.00	29.11	A
ATOM	1886	CG2	VAL	A	241	-9.321	18.326	55.911	1.00	24.66	A
ATOM	1887	C	VAL	A	241	-9.175	19.896	53.466	1.00	23.84	A
ATOM	1888	O	VAL	A	241	-8.040	19.720	53.031	1.00	21.96	A
ATOM	1889	N	SER	A	242	-9.625	21.078	53.856	1.00	24.95	A
ATOM	1890	CA	SER	A	242	-8.778	22.261	53.886	1.00	27.82	A
ATOM	1891	CB	SER	A	242	-9.072	23.180	52.708	1.00	27.02	A
ATOM	1892	OG	SER	A	242	-8.219	24.310	52.761	1.00	27.89	A
ATOM	1893	C	SER	A	242	-9.173	22.938	55.202	1.00	26.21	A
ATOM	1894	O	SER	A	242	-10.000	23.844	55.212	1.00	26.14	A
ATOM	1895	N	TRP	A	243	-8.587	22.477	56.303	1.00	25.81	A
ATOM	1896	CA	TRP	A	243	-8.907	23.003	57.624	1.00	28.94	A
ATOM	1897	CB	TRP	A	243	-9.466	21.903	58.536	1.00	28.32	A
ATOM	1898	CG	TRP	A	243	-10.735	21.232	58.139	1.00	24.34	A
ATOM	1899	CD2	TRP	A	243	-11.254	20.029	58.706	1.00	26.28	A
ATOM	1900	CE2	TRP	A	243	-12.501	19.785	58.100	1.00	27.40	A
ATOM	1901	CE3	TRP	A	243	-10.782	19.129	59.675	1.00	33.54	A
ATOM	1902	CD1	TRP	A	243	-11.659	21.662	57.235	1.00	26.89	A
ATOM	1903	NE1	TRP	A	243	-12.727	20.797	57.204	1.00	25.72	A
ATOM	1904	CZ2	TRP	A	243	-13.289	18.677	58.430	1.00	31.19	A
ATOM	1905	CZ3	TRP	A	243	-11.569	18.025	60.001	1.00	29.42	A
ATOM	1906	CH2	TRP	A	243	-12.805	17.812	59.378	1.00	26.13	A
ATOM	1907	C	TRP	A	243	-7.739	23.588	58.390	1.00	27.27	A
ATOM	1908	O	TRP	A	243	-6.578	23.364	58.060	1.00	24.46	A
ATOM	1909	N	TYR	A	244	-8.090	24.327	59.440	1.00	27.14	A
ATOM	1910	CA	TYR	A	244	-7.139	24.904	60.380	1.00	27.59	A
ATOM	1911	CB	TYR	A	244	-6.302	23.773	60.971	1.00	25.82	A
ATOM	1912	CG	TYR	A	244	-7.119	22.609	61.476	1.00	33.08	A
ATOM	1913	CD1	TYR	A	244	-6.746	21.296	61.182	1.00	34.75	A
ATOM	1914	CE1	TYR	A	244	-7.481	20.211	61.658	1.00	30.72	A
ATOM	1915	CD2	TYR	A	244	-8.255	22.811	62.264	1.00	31.38	A
ATOM	1916	CE2	TYR	A	244	-8.996	21.739	62.746	1.00	34.32	A
ATOM	1917	CZ	TYR	A	244	-8.606	20.438	62.441	1.00	38.44	A
ATOM	1918	OH	TYR	A	244	-9.341	19.369	62.916	1.00	33.27	A
ATOM	1919	C	TYR	A	244	-6.205	26.031	59.959	1.00	26.41	A
ATOM	1920	O	TYR	A	244	-5.357	26.434	60.751	1.00	30.28	A

ATOM	1921	N	SER	A	245	-6.328	26.542	58.741	1.00	25.31	A
ATOM	1922	CA	SER	A	245	-5.453	27.637	58.328	1.00	25.94	A
ATOM	1923	CB	SER	A	245	-4.468	27.173	57.247	1.00	28.65	A
ATOM	1924	OG	SER	A	245	-3.485	26.305	57.793	1.00	27.86	A
ATOM	1925	C	SER	A	245	-6.234	28.858	57.844	1.00	29.95	A
ATOM	1926	O	SER	A	245	-7.391	28.754	57.433	1.00	25.58	A
ATOM	1927	N	SER	A	246	-5.589	30.018	57.910	1.00	28.72	A
ATOM	1928	CA	SER	A	246	-6.191	31.280	57.494	1.00	29.87	A
ATOM	1929	CB	SER	A	246	-5.264	32.435	57.863	1.00	30.51	A
ATOM	1930	OG	SER	A	246	-3.958	32.211	57.346	1.00	41.80	A
ATOM	1931	C	SER	A	246	-6.507	31.328	55.998	1.00	28.94	A
ATOM	1932	O	SER	A	246	-7.444	32.006	55.582	1.00	26.44	A
ATOM	1933	N	SER	A	247	-5.713	30.627	55.194	1.00	25.00	A
ATOM	1934	CA	SER	A	247	-5.939	30.573	53.745	1.00	29.18	A
ATOM	1935	CB	SER	A	247	-4.728	31.112	52.973	1.00	29.94	A
ATOM	1936	OG	SER	A	247	-4.638	32.521	53.056	1.00	38.70	A
ATOM	1937	C	SER	A	247	-6.198	29.132	53.322	1.00	24.86	A
ATOM	1938	O	SER	A	247	-5.580	28.200	53.834	1.00	26.50	A
ATOM	1939	N	PRO	A	248	-7.120	28.930	52.379	1.00	26.33	A
ATOM	1940	CD	PRO	A	248	-8.056	29.891	51.770	1.00	29.46	A
ATOM	1941	CA	PRO	A	248	-7.408	27.570	51.940	1.00	27.61	A
ATOM	1942	CB	PRO	A	248	-8.744	27.725	51.221	1.00	30.78	A
ATOM	1943	CG	PRO	A	248	-8.655	29.094	50.647	1.00	32.87	A
ATOM	1944	C	PRO	A	248	-6.336	26.949	51.047	1.00	30.21	A
ATOM	1945	O	PRO	A	248	-5.508	27.650	50.462	1.00	20.35	A
ATOM	1946	N	GLY	A	249	-6.358	25.618	50.983	1.00	26.55	A
ATOM	1947	CA	GLY	A	249	-5.441	24.884	50.136	1.00	26.90	A
ATOM	1948	C	GLY	A	249	-6.300	24.356	49.002	1.00	28.34	A
ATOM	1949	O	GLY	A	249	-7.527	24.335	49.133	1.00	26.16	A
ATOM	1950	N	TYR	A	250	-5.689	23.927	47.901	1.00	23.14	A
ATOM	1951	CA	TYR	A	250	-6.464	23.431	46.766	1.00	24.57	A
ATOM	1952	CB	TYR	A	250	-6.245	24.327	45.543	1.00	22.59	A
ATOM	1953	CG	TYR	A	250	-6.476	25.784	45.841	1.00	28.67	A
ATOM	1954	CD1	TYR	A	250	-5.419	26.623	46.188	1.00	29.48	A
ATOM	1955	CE1	TYR	A	250	-5.639	27.936	46.567	1.00	31.35	A
ATOM	1956	CD2	TYR	A	250	-7.764	26.305	45.873	1.00	32.49	A
ATOM	1957	CE2	TYR	A	250	-7.998	27.611	46.252	1.00	32.13	A
ATOM	1958	CZ	TYR	A	250	-6.933	28.423	46.602	1.00	35.99	A
ATOM	1959	OH	TYR	A	250	-7.187	29.713	47.009	1.00	40.28	A
ATOM	1960	C	TYR	A	250	-6.151	21.991	46.390	1.00	23.78	A
ATOM	1961	O	TYR	A	250	-5.181	21.406	46.873	1.00	20.76	A
ATOM	1962	N	TRP	A	251	-6.986	21.429	45.522	1.00	19.34	A
ATOM	1963	CA	TRP	A	251	-6.779	20.070	45.067	1.00	20.03	A
ATOM	1964	CB	TRP	A	251	-7.393	19.064	46.054	1.00	20.29	A
ATOM	1965	CG	TRP	A	251	-8.830	19.318	46.390	1.00	20.84	A
ATOM	1966	CD2	TRP	A	251	-9.340	19.762	47.653	1.00	25.16	A
ATOM	1967	CE2	TRP	A	251	-10.742	19.878	47.522	1.00	26.95	A
ATOM	1968	CE3	TRP	A	251	-8.745	20.073	48.885	1.00	25.11	A
ATOM	1969	CD1	TRP	A	251	-9.911	19.186	45.565	1.00	22.83	A
ATOM	1970	NE1	TRP	A	251	-11.065	19.522	46.238	1.00	25.67	A
ATOM	1971	CZ2	TRP	A	251	-11.560	20.292	48.579	1.00	30.64	A
ATOM	1972	CZ3	TRP	A	251	-9.559	20.486	49.938	1.00	29.51	A
ATOM	1973	CH2	TRP	A	251	-10.954	20.590	49.776	1.00	28.14	A
ATOM	1974	C	TRP	A	251	-7.322	19.807	43.674	1.00	23.68	A
ATOM	1975	O	TRP	A	251	-8.346	20.359	43.260	1.00	22.93	A
ATOM	1976	N	HIS	A	252	-6.599	18.965	42.952	1.00	21.15	A
ATOM	1977	CA	HIS	A	252	-6.989	18.552	41.627	1.00	20.95	A
ATOM	1978	CB	HIS	A	252	-5.863	18.846	40.634	1.00	20.31	A
ATOM	1979	CG	HIS	A	252	-6.179	18.472	39.217	1.00	21.82	A
ATOM	1980	CD2	HIS	A	252	-7.052	17.575	38.701	1.00	21.05	A
ATOM	1981	ND1	HIS	A	252	-5.520	19.025	38.140	1.00	21.90	A
ATOM	1982	CE1	HIS	A	252	-5.972	18.484	37.023	1.00	22.28	A
ATOM	1983	NE2	HIS	A	252	-6.902	17.601	37.335	1.00	20.22	A
ATOM	1984	C	HIS	A	252	-7.192	17.059	41.835	1.00	22.82	A
ATOM	1985	O	HIS	A	252	-6.227	16.299	41.920	1.00	23.22	A
ATOM	1986	N	VAL	A	253	-8.451	16.654	41.964	1.00	23.82	A
ATOM	1987	CA	VAL	A	253	-8.782	15.259	42.202	1.00	25.43	A
ATOM	1988	CB	VAL	A	253	-9.916	15.107	43.241	1.00	27.09	A
ATOM	1989	CG1	VAL	A	253	-9.451	15.613	44.597	1.00	25.70	A

ATOM	1990	CG2	VAL	A	253	-11.155	15.859	42.776	1.00	29.06	A
ATOM	1991	C	VAL	A	253	-9.201	14.528	40.941	1.00	29.50	A
ATOM	1992	O	VAL	A	253	-9.710	15.128	39.986	1.00	22.22	A
ATOM	1993	N	SER	A	254	-8.979	13.221	40.954	1.00	26.50	A
ATOM	1994	CA	SER	A	254	-9.335	12.383	39.827	1.00	27.23	A
ATOM	1995	CB	SER	A	254	-8.378	12.612	38.660	1.00	31.48	A
ATOM	1996	OG	SER	A	254	-8.671	11.709	37.608	1.00	34.90	A
ATOM	1997	C	SER	A	254	-9.344	10.907	40.173	1.00	26.91	A
ATOM	1998	O	SER	A	254	-8.367	10.358	40.688	1.00	21.99	A
ATOM	1999	N	ASN	A	255	-10.476	10.277	39.890	1.00	27.94	A
ATOM	2000	CA	ASN	A	255	-10.657	8.859	40.104	1.00	25.53	A
ATOM	2001	CB	ASN	A	255	-9.994	8.100	38.959	1.00	32.79	A
ATOM	2002	CG	ASN	A	255	-10.364	6.638	38.944	1.00	39.05	A
ATOM	2003	OD1	ASN	A	255	-11.457	6.256	39.381	1.00	38.05	A
ATOM	2004	ND2	ASN	A	255	-9.461	5.804	38.430	1.00	41.64	A
ATOM	2005	C	ASN	A	255	-10.182	8.306	41.449	1.00	28.87	A
ATOM	2006	O	ASN	A	255	-9.361	7.397	41.504	1.00	26.55	A
ATOM	2007	N	ASN	A	256	-10.695	8.870	42.534	1.00	25.90	A
ATOM	2008	CA	ASN	A	256	-10.365	8.379	43.867	1.00	26.88	A
ATOM	2009	CB	ASN	A	256	-10.164	9.532	44.859	1.00	26.24	A
ATOM	2010	CG	ASN	A	256	-8.856	10.271	44.638	1.00	23.62	A
ATOM	2011	OD1	ASN	A	256	-7.776	9.702	44.778	1.00	20.26	A
ATOM	2012	ND2	ASN	A	256	-8.952	11.549	44.283	1.00	23.69	A
ATOM	2013	C	ASN	A	256	-11.551	7.533	44.312	1.00	26.53	A
ATOM	2014	O	ASN	A	256	-12.690	7.811	43.943	1.00	28.52	A
ATOM	2015	N	LYS	A	257	-11.289	6.505	45.103	1.00	27.28	A
ATOM	2016	CA	LYS	A	257	-12.365	5.651	45.571	1.00	29.67	A
ATOM	2017	CB	LYS	A	257	-12.122	4.208	45.114	1.00	30.13	A
ATOM	2018	CG	LYS	A	257	-13.334	3.316	45.272	1.00	35.82	A
ATOM	2019	CD	LYS	A	257	-13.195	2.028	44.472	1.00	40.34	A
ATOM	2020	CE	LYS	A	257	-14.544	1.307	44.385	1.00	45.92	A
ATOM	2021	NZ	LYS	A	257	-14.570	.283	43.300	1.00	45.80	A
ATOM	2022	C	LYS	A	257	-12.517	5.707	47.087	1.00	28.28	A
ATOM	2023	O	LYS	A	257	-11.552	5.519	47.832	1.00	28.10	A
ATOM	2024	N	PHE	A	258	-13.736	5.978	47.538	1.00	27.49	A
ATOM	2025	CA	PHE	A	258	-14.022	6.050	48.968	1.00	28.58	A
ATOM	2026	CB	PHE	A	258	-14.726	7.366	49.310	1.00	29.89	A
ATOM	2027	CG	PHE	A	258	-14.030	8.586	48.772	1.00	29.51	A
ATOM	2028	CD1	PHE	A	258	-14.296	9.045	47.483	1.00	28.03	A
ATOM	2029	CD2	PHE	A	258	-13.086	9.259	49.541	1.00	30.34	A
ATOM	2030	CE1	PHE	A	258	-13.632	10.156	46.970	1.00	31.31	A
ATOM	2031	CE2	PHE	A	258	-12.414	10.374	49.038	1.00	30.25	A
ATOM	2032	CZ	PHE	A	258	-12.688	10.822	47.751	1.00	30.78	A
ATOM	2033	C	PHE	A	258	-14.906	4.874	49.384	1.00	28.35	A
ATOM	2034	O	PHE	A	258	-15.982	4.673	48.832	1.00	28.20	A
ATOM	2035	N	VAL	A	259	-14.445	4.100	50.359	1.00	30.00	A
ATOM	2036	CA	VAL	A	259	-15.193	2.943	50.830	1.00	33.86	A
ATOM	2037	CB	VAL	A	259	-14.433	1.630	50.523	1.00	33.76	A
ATOM	2038	CG1	VAL	A	259	-15.239	.432	50.994	1.00	31.77	A
ATOM	2039	CG2	VAL	A	259	-14.168	1.529	49.036	1.00	32.62	A
ATOM	2040	C	VAL	A	259	-15.446	3.041	52.328	1.00	34.06	A
ATOM	2041	O	VAL	A	259	-14.513	3.202	53.115	1.00	35.14	A
ATOM	2042	N	ASN	A	260	-16.714	2.931	52.718	1.00	34.44	A
ATOM	2043	CA	ASN	A	260	-17.092	3.028	54.125	1.00	36.76	A
ATOM	2044	CB	ASN	A	260	-16.670	1.773	54.890	1.00	43.66	A
ATOM	2045	CG	ASN	A	260	-17.631	.629	54.688	1.00	52.65	A
ATOM	2046	OD1	ASN	A	260	-18.847	.814	54.775	1.00	59.18	A
ATOM	2047	ND2	ASN	A	260	-17.100	-.566	54.430	1.00	54.78	A
ATOM	2048	C	ASN	A	260	-16.456	4.250	54.762	1.00	34.06	A
ATOM	2049	O	ASN	A	260	-15.950	4.195	55.882	1.00	29.45	A
ATOM	2050	N	SER	A	261	-16.488	5.352	54.028	1.00	34.37	A
ATOM	2051	CA	SER	A	261	-15.922	6.601	54.495	1.00	36.33	A
ATOM	2052	CB	SER	A	261	-14.869	7.091	53.495	1.00	30.37	A
ATOM	2053	OG	SER	A	261	-13.835	6.133	53.343	1.00	29.11	A
ATOM	2054	C	SER	A	261	-17.034	7.633	54.634	1.00	36.66	A
ATOM	2055	O	SER	A	261	-18.101	7.494	54.036	1.00	37.04	A
ATOM	2056	N	ARG	A	262	-16.782	8.667	55.426	1.00	35.39	A
ATOM	2057	CA	ARG	A	262	-17.770	9.723	55.621	1.00	36.84	A
ATOM	2058	CB	ARG	A	262	-18.581	9.469	56.882	1.00	40.66	A

ATOM	2059	CG	ARG	A	262	-17.722	9.300	58.115	1.00	43.81	A
ATOM	2060	CD	ARG	A	262	-17.859	7.892	58.677	1.00	52.39	A
ATOM	2061	NE	ARG	A	262	-16.937	7.629	59.786	1.00	56.18	A
ATOM	2062	CZ	ARG	A	262	-16.818	8.399	60.869	1.00	57.27	A
ATOM	2063	NH1	ARG	A	262	-17.561	9.497	60.998	1.00	55.24	A
ATOM	2064	NH2	ARG	A	262	-15.961	8.063	61.834	1.00	54.82	A
ATOM	2065	C	ARG	A	262	-17.091	11.076	55.736	1.00	35.15	A
ATOM	2066	O	ARG	A	262	-15.876	11.161	55.915	1.00	30.12	A
ATOM	2067	N	GLY	A	263	-17.886	12.135	55.640	1.00	34.17	A
ATOM	2068	CA	GLY	A	263	-17.333	13.467	55.746	1.00	32.70	A
ATOM	2069	C	GLY	A	263	-16.957	14.035	54.396	1.00	28.85	A
ATOM	2070	O	GLY	A	263	-17.571	13.716	53.387	1.00	28.95	A
ATOM	2071	N	SER	A	264	-15.934	14.876	54.377	1.00	30.16	A
ATOM	2072	CA	SER	A	264	-15.484	15.507	53.145	1.00	30.06	A
ATOM	2073	CB	SER	A	264	-14.503	16.635	53.491	1.00	28.87	A
ATOM	2074	OG	SER	A	264	-14.188	17.408	52.348	1.00	35.14	A
ATOM	2075	C	SER	A	264	-14.837	14.516	52.167	1.00	27.54	A
ATOM	2076	O	SER	A	264	-13.780	13.951	52.449	1.00	27.44	A
ATOM	2077	N	MET	A	265	-15.477	14.324	51.015	1.00	29.88	A
ATOM	2078	CA	MET	A	265	-14.981	13.409	49.983	1.00	32.08	A
ATOM	2079	CB	MET	A	265	-15.766	12.093	50.020	1.00	30.49	A
ATOM	2080	CG	MET	A	265	-15.626	11.347	51.330	1.00	37.31	A
ATOM	2081	SD	MET	A	265	-16.735	9.921	51.478	1.00	40.46	A
ATOM	2082	CE	MET	A	265	-18.226	10.735	52.014	1.00	41.13	A
ATOM	2083	C	MET	A	265	-15.171	14.081	48.633	1.00	31.45	A
ATOM	2084	O	MET	A	265	-15.955	13.617	47.807	1.00	29.13	A
ATOM	2085	N	PRO	A	266	-14.441	15.186	48.390	1.00	32.82	A
ATOM	2086	CD	PRO	A	266	-13.381	15.704	49.276	1.00	33.76	A
ATOM	2087	CA	PRO	A	266	-14.505	15.965	47.149	1.00	32.10	A
ATOM	2088	CB	PRO	A	266	-13.416	17.021	47.342	1.00	33.53	A
ATOM	2089	CG	PRO	A	266	-13.281	17.133	48.835	1.00	38.84	A
ATOM	2090	C	PRO	A	266	-14.265	15.152	45.881	1.00	31.43	A
ATOM	2091	O	PRO	A	266	-13.338	14.351	45.822	1.00	29.33	A
ATOM	2092	N	THR	A	267	-15.102	15.360	44.871	1.00	28.49	A
ATOM	2093	CA	THR	A	267	-14.931	14.670	43.598	1.00	33.15	A
ATOM	2094	CB	THR	A	267	-16.146	13.788	43.230	1.00	34.23	A
ATOM	2095	OG1	THR	A	267	-17.294	14.617	43.009	1.00	37.49	A
ATOM	2096	CG2	THR	A	267	-16.449	12.804	44.342	1.00	35.82	A
ATOM	2097	C	THR	A	267	-14.752	15.737	42.526	1.00	34.29	A
ATOM	2098	O	THR	A	267	-14.602	15.432	41.351	1.00	34.85	A
ATOM	2099	N	THR	A	268	-14.785	16.998	42.944	1.00	30.97	A
ATOM	2100	CA	THR	A	268	-14.598	18.113	42.026	1.00	32.84	A
ATOM	2101	CB	THR	A	268	-15.815	19.076	42.045	1.00	35.83	A
ATOM	2102	OG1	THR	A	268	-16.205	19.320	43.399	1.00	42.15	A
ATOM	2103	CG2	THR	A	268	-16.994	18.471	41.295	1.00	39.82	A
ATOM	2104	C	THR	A	268	-13.334	18.854	42.456	1.00	30.79	A
ATOM	2105	O	THR	A	268	-13.045	18.967	43.646	1.00	26.42	A
ATOM	2106	N	SER	A	269	-12.585	19.356	41.481	1.00	27.47	A
ATOM	2107	CA	SER	A	269	-11.329	20.050	41.758	1.00	28.01	A
ATOM	2108	CB	SER	A	269	-10.355	19.810	40.603	1.00	27.31	A
ATOM	2109	OG	SER	A	269	-10.294	18.429	40.281	1.00	24.27	A
ATOM	2110	C	SER	A	269	-11.468	21.548	42.002	1.00	30.07	A
ATOM	2111	O	SER	A	269	-12.324	22.205	41.414	1.00	32.94	A
ATOM	2112	N	THR	A	270	-10.622	22.083	42.876	1.00	27.01	A
ATOM	2113	CA	THR	A	270	-10.638	23.507	43.186	1.00	27.02	A
ATOM	2114	CB	THR	A	270	-10.689	23.754	44.705	1.00	25.49	A
ATOM	2115	OG1	THR	A	270	-9.611	23.059	45.335	1.00	24.38	A
ATOM	2116	CG2	THR	A	270	-12.006	23.262	45.279	1.00	23.39	A
ATOM	2117	C	THR	A	270	-9.398	24.190	42.610	1.00	28.16	A
ATOM	2118	O	THR	A	270	-9.085	25.331	42.956	1.00	29.02	A
ATOM	2119	N	THR	A	271	-8.682	23.472	41.751	1.00	25.27	A
ATOM	2120	CA	THR	A	271	-7.501	24.014	41.094	1.00	25.29	A
ATOM	2121	CB	THR	A	271	-6.338	24.277	42.073	1.00	26.55	A
ATOM	2122	OG1	THR	A	271	-5.373	25.125	41.439	1.00	21.88	A
ATOM	2123	CG2	THR	A	271	-5.647	22.975	42.456	1.00	27.58	A
ATOM	2124	C	THR	A	271	-7.006	23.039	40.049	1.00	25.54	A
ATOM	2125	O	THR	A	271	-7.372	21.870	40.059	1.00	24.89	A
ATOM	2126	N	THR	A	272	-6.179	23.536	39.141	1.00	23.11	A
ATOM	2127	CA	THR	A	272	-5.605	22.699	38.108	1.00	25.14	A

ATOM	2128	CB	THR	A	272	-5.800	23.307	36.700	1.00	28.58	A
ATOM	2129	OG1	THR	A	272	-7.191	23.309	36.357	1.00	27.70	A
ATOM	2130	CG2	THR	A	272	-5.042	22.497	35.668	1.00	27.82	A
ATOM	2131	C	THR	A	272	-4.110	22.550	38.377	1.00	29.23	A
ATOM	2132	O	THR	A	272	-3.374	23.533	38.420	1.00	24.37	A
ATOM	2133	N	TYR	A	273	-3.663	21.320	38.592	1.00	25.89	A
ATOM	2134	CA	TYR	A	273	-2.250	21.085	38.824	1.00	24.99	A
ATOM	2135	CB	TYR	A	273	-1.933	21.016	40.312	1.00	24.00	A
ATOM	2136	CG	TYR	A	273	-.455	20.837	40.560	1.00	26.27	A
ATOM	2137	CD1	TYR	A	273	.454	21.822	40.182	1.00	24.51	A
ATOM	2138	CE1	TYR	A	273	1.831	21.622	40.309	1.00	23.59	A
ATOM	2139	CD2	TYR	A	273	.047	19.644	41.084	1.00	23.94	A
ATOM	2140	CE2	TYR	A	273	1.422	19.434	41.211	1.00	24.12	A
ATOM	2141	CZ	TYR	A	273	2.305	20.428	40.818	1.00	26.72	A
ATOM	2142	OH	TYR	A	273	3.660	20.221	40.909	1.00	23.30	A
ATOM	2143	C	TYR	A	273	-1.790	19.801	38.145	1.00	27.56	A
ATOM	2144	O	TYR	A	273	-2.343	18.724	38.377	1.00	21.79	A
ATOM	2145	N	ASN	A	274	-.780	19.939	37.293	1.00	26.73	A
ATOM	2146	CA	ASN	A	274	-.215	18.815	36.558	1.00	27.82	A
ATOM	2147	CB	ASN	A	274	-.276	19.065	35.048	1.00	28.89	A
ATOM	2148	CG	ASN	A	274	-1.676	19.379	34.560	1.00	33.35	A
ATOM	2149	OD1	ASN	A	274	-2.610	18.601	34.764	1.00	33.86	A
ATOM	2150	ND2	ASN	A	274	-1.826	20.526	33.906	1.00	32.07	A
ATOM	2151	C	ASN	A	274	1.237	18.666	36.982	1.00	28.18	A
ATOM	2152	O	ASN	A	274	2.046	19.563	36.762	1.00	25.68	A
ATOM	2153	N	PRO	A	275	1.583	17.533	37.611	1.00	28.36	A
ATOM	2154	CD	PRO	A	275	.728	16.412	38.036	1.00	26.11	A
ATOM	2155	CA	PRO	A	275	2.967	17.332	38.044	1.00	26.76	A
ATOM	2156	CB	PRO	A	275	2.936	15.939	38.665	1.00	28.99	A
ATOM	2157	CG	PRO	A	275	1.530	15.825	39.182	1.00	29.12	A
ATOM	2158	C	PRO	A	275	3.913	17.417	36.851	1.00	26.57	A
ATOM	2159	O	PRO	A	275	3.615	16.913	35.778	1.00	24.87	A
ATOM	2160	N	PRO	A	276	5.065	18.073	37.030	1.00	27.28	A
ATOM	2161	CD	PRO	A	276	5.399	18.848	38.235	1.00	31.49	A
ATOM	2162	CA	PRO	A	276	6.089	18.255	36.000	1.00	29.92	A
ATOM	2163	CB	PRO	A	276	6.900	19.429	36.538	1.00	27.26	A
ATOM	2164	CG	PRO	A	276	6.858	19.187	38.005	1.00	32.63	A
ATOM	2165	C	PRO	A	276	6.971	17.032	35.702	1.00	30.14	A
ATOM	2166	O	PRO	A	276	8.176	17.158	35.508	1.00	31.18	A
ATOM	2167	N	TYR	A	277	6.376	15.850	35.679	1.00	29.20	A
ATOM	2168	CA	TYR	A	277	7.121	14.633	35.377	1.00	24.17	A
ATOM	2169	CB	TYR	A	277	7.858	14.102	36.610	1.00	26.40	A
ATOM	2170	CG	TYR	A	277	7.023	14.015	37.865	1.00	22.56	A
ATOM	2171	CD1	TYR	A	277	7.165	14.963	38.878	1.00	21.60	A
ATOM	2172	CE1	TYR	A	277	6.387	14.911	40.036	1.00	20.55	A
ATOM	2173	CD2	TYR	A	277	6.080	13.003	38.035	1.00	20.04	A
ATOM	2174	CE2	TYR	A	277	5.296	12.936	39.184	1.00	23.64	A
ATOM	2175	CZ	TYR	A	277	5.455	13.896	40.182	1.00	22.56	A
ATOM	2176	OH	TYR	A	277	4.691	13.848	41.319	1.00	21.13	A
ATOM	2177	C	TYR	A	277	6.141	13.590	34.897	1.00	26.17	A
ATOM	2178	O	TYR	A	277	4.936	13.711	35.125	1.00	21.33	A
ATOM	2179	N	SER	A	278	6.640	12.561	34.227	1.00	23.88	A
ATOM	2180	CA	SER	A	278	5.739	11.530	33.759	1.00	21.44	A
ATOM	2181	CB	SER	A	278	6.277	10.873	32.493	1.00	27.50	A
ATOM	2182	OG	SER	A	278	7.367	10.027	32.783	1.00	30.01	A
ATOM	2183	C	SER	A	278	5.595	10.496	34.863	1.00	22.21	A
ATOM	2184	O	SER	A	278	6.437	10.404	35.758	1.00	20.59	A
ATOM	2185	N	TYR	A	279	4.514	9.731	34.803	1.00	21.21	A
ATOM	2186	CA	TYR	A	279	4.256	8.691	35.783	1.00	22.81	A
ATOM	2187	CB	TYR	A	279	3.873	9.306	37.140	1.00	24.00	A
ATOM	2188	CG	TYR	A	279	2.660	10.211	37.087	1.00	19.88	A
ATOM	2189	CD1	TYR	A	279	2.776	11.542	36.695	1.00	23.76	A
ATOM	2190	CE1	TYR	A	279	1.661	12.376	36.625	1.00	25.52	A
ATOM	2191	CD2	TYR	A	279	1.393	9.729	37.410	1.00	19.40	A
ATOM	2192	CE2	TYR	A	279	.271	10.550	37.343	1.00	21.38	A
ATOM	2193	CZ	TYR	A	279	.415	11.871	36.951	1.00	23.93	A
ATOM	2194	OH	TYR	A	279	-.678	12.687	36.894	1.00	23.53	A
ATOM	2195	C	TYR	A	279	3.129	7.794	35.288	1.00	24.43	A
ATOM	2196	O	TYR	A	279	2.335	8.194	34.441	1.00	25.42	A

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ATOM   2197  N   SER A 280       3.067   6.576  35.817  1.00 28.96      A
ATOM   2198  CA  SER A 280       2.030   5.620  35.442  1.00 30.09      A
ATOM   2199  CB  SER A 280       2.643   4.279  35.055  1.00 31.83      A
ATOM   2200  OG  SER A 280       3.657   4.455  34.088  1.00 42.74      A
ATOM   2201  C   SER A 280       1.115   5.400  36.625  1.00 29.18      A
ATOM   2202  O   SER A 280       1.571   5.232  37.753  1.00 29.97      A
ATOM   2203  N   LEU A 281       -.180   5.382  36.355  1.00 27.49      A
ATOM   2204  CA  LEU A 281      -1.166   5.186  37.399  1.00 26.85      A
ATOM   2205  CB  LEU A 281      -2.298   6.205  37.246  1.00 25.05      A
ATOM   2206  CG  LEU A 281      -2.023   7.658  37.636  1.00 24.75      A
ATOM   2207  CD1 LEU A 281      -3.258   8.486  37.375  1.00 24.54      A
ATOM   2208  CD2 LEU A 281      -1.646   7.737  39.103  1.00 19.68      A
ATOM   2209  C   LEU A 281      -1.760   3.780  37.385  1.00 27.46      A
ATOM   2210  O   LEU A 281      -2.242   3.315  36.357  1.00 21.15      A
ATOM   2211  N   ASP A 282      -1.716   3.107  38.529  1.00 24.91      A
ATOM   2212  CA  ASP A 282      -2.293   1.777  38.648  1.00 23.90      A
ATOM   2213  CB  ASP A 282      -1.794   1.055  39.906  1.00 25.34      A
ATOM   2214  CG  ASP A 282       -.360    .573  39.781  1.00 27.69      A
ATOM   2215  OD1 ASP A 282       -.021   -.015  38.738  1.00 31.69      A
ATOM   2216  OD2 ASP A 282        .423    .766  40.732  1.00 28.26      A
ATOM   2217  C   ASP A 282      -3.792   1.976  38.781  1.00 28.83      A
ATOM   2218  O   ASP A 282      -4.240   3.021  39.244  1.00 25.09      A
ATOM   2219  N   ASN A 283      -4.561    .974  38.367  1.00 30.71      A
ATOM   2220  CA  ASN A 283      -6.019   1.013  38.464  1.00 31.24      A
ATOM   2221  CB  ASN A 283      -6.607   -.296  37.931  1.00 37.48      A
ATOM   2222  CG  ASN A 283      -8.124   -.306  37.945  1.00 50.02      A
ATOM   2223  OD1 ASN A 283      -8.760    .216  38.869  1.00 54.12      A
ATOM   2224  ND2 ASN A 283      -8.720   -.915  36.922  1.00 58.66      A
ATOM   2225  C   ASN A 283      -6.370   1.164  39.946  1.00 26.47      A
ATOM   2226  O   ASN A 283      -5.831    .454  40.791  1.00 25.43      A
ATOM   2227  N   VAL A 284      -7.278   2.073  40.266  1.00 27.83      A
ATOM   2228  CA  VAL A 284      -7.642   2.293  41.665  1.00 31.08      A
ATOM   2229  CB  VAL A 284      -8.745   3.380  41.793  1.00 30.78      A
ATOM   2230  CG1 VAL A 284     -10.092   2.841  41.324  1.00 30.53      A
ATOM   2231  CG2 VAL A 284      -8.827   3.863  43.223  1.00 32.72      A
ATOM   2232  C   VAL A 284      -8.107   1.004  42.350  1.00 33.85      A
ATOM   2233  O   VAL A 284      -7.947    .840  43.561  1.00 32.70      A
ATOM   2234  N   ASP A 285      -8.671    .086  41.572  1.00 34.76      A
ATOM   2235  CA  ASP A 285      -9.147  -1.185  42.106  1.00 36.04      A
ATOM   2236  CB  ASP A 285     -10.074  -1.878  41.100  1.00 40.69      A
ATOM   2237  CG  ASP A 285     -11.507  -1.392  41.195  1.00 51.41      A
ATOM   2238  OD1 ASP A 285     -11.801   -.256  40.755  1.00 56.02      A
ATOM   2239  OD2 ASP A 285     -12.350  -2.152  41.729  1.00 59.77      A
ATOM   2240  C   ASP A 285      -8.034  -2.153  42.482  1.00 35.69      A
ATOM   2241  O   ASP A 285      -8.272  -3.114  43.206  1.00 36.29      A
ATOM   2242  N   ASN A 286      -6.819  -1.903  42.008  1.00 30.36      A
ATOM   2243  CA  ASN A 286      -5.697  -2.797  42.293  1.00 29.63      A
ATOM   2244  CB  ASN A 286      -4.880  -3.037  41.013  1.00 33.33      A
ATOM   2245  CG  ASN A 286      -5.698  -3.658  39.903  1.00 41.80      A
ATOM   2246  OD1 ASN A 286      -5.295  -3.644  38.731  1.00 45.29      A
ATOM   2247  ND2 ASN A 286      -6.852  -4.215  40.257  1.00 45.08      A
ATOM   2248  C   ASN A 286      -4.765  -2.277  43.372  1.00 27.84      A
ATOM   2249  O   ASN A 286      -3.889  -3.002  43.838  1.00 29.28      A
ATOM   2250  N   VAL A 287      -4.957  -1.019  43.755  1.00 26.64      A
ATOM   2251  CA  VAL A 287      -4.126   -.364  44.760  1.00 26.01      A
ATOM   2252  CB  VAL A 287      -4.679   1.048  45.081  1.00 26.33      A
ATOM   2253  CG1 VAL A 287      -3.952   1.645  46.278  1.00 31.79      A
ATOM   2254  CG2 VAL A 287      -4.518   1.947  43.859  1.00 24.26      A
ATOM   2255  C   VAL A 287      -3.939  -1.123  46.070  1.00 28.18      A
ATOM   2256  O   VAL A 287      -2.807  -1.359  46.506  1.00 24.64      A
ATOM   2257  N   LYS A 288      -5.047  -1.494  46.699  1.00 23.95      A
ATOM   2258  CA  LYS A 288      -4.995  -2.206  47.963  1.00 28.30      A
ATOM   2259  CB  LYS A 288      -6.403  -2.649  48.370  1.00 29.27      A
ATOM   2260  CG  LYS A 288      -6.480  -3.278  49.754  1.00 33.22      A
ATOM   2261  CD  LYS A 288      -7.933  -3.451  50.180  1.00 33.21      A
ATOM   2262  CE  LYS A 288      -8.034  -4.073  51.559  1.00 40.32      A
ATOM   2263  NZ  LYS A 288      -9.458  -4.231  51.970  1.00 38.15      A
ATOM   2264  C   LYS A 288      -4.076  -3.418  47.897  1.00 27.52      A
ATOM   2265  O   LYS A 288      -3.142  -3.554  48.684  1.00 25.83      A
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ATOM	2266	N	SER	A	289	-4.351	-4.294	46.943	1.00	31.46	A
ATOM	2267	CA	SER	A	289	-3.577	-5.511	46.752	1.00	31.17	A
ATOM	2268	CB	SER	A	289	-4.176	-6.305	45.586	1.00	33.54	A
ATOM	2269	OG	SER	A	289	-3.448	-7.490	45.336	1.00	33.41	A
ATOM	2270	C	SER	A	289	-2.081	-5.257	46.497	1.00	30.07	A
ATOM	2271	O	SER	A	289	-1.221	-5.909	47.090	1.00	27.24	A
ATOM	2272	N	ILE	A	290	-1.773	-4.312	45.618	1.00	24.38	A
ATOM	2273	CA	ILE	A	290	-.383	-4.016	45.296	1.00	23.78	A
ATOM	2274	CB	ILE	A	290	-.296	-3.081	44.076	1.00	25.24	A
ATOM	2275	CG2	ILE	A	290	1.143	-2.645	43.848	1.00	23.99	A
ATOM	2276	CG1	ILE	A	290	-.852	-3.801	42.844	1.00	24.23	A
ATOM	2277	CD1	ILE	A	290	-.923	-2.933	41.599	1.00	30.48	A
ATOM	2278	C	ILE	A	290	.396	-3.405	46.456	1.00	23.85	A
ATOM	2279	O	ILE	A	290	1.519	-3.809	46.740	1.00	25.66	A
ATOM	2280	N	VAL	A	291	-.206	-2.429	47.125	1.00	22.61	A
ATOM	2281	CA	VAL	A	291	.437	-1.752	48.239	1.00	22.28	A
ATOM	2282	CB	VAL	A	291	-.359	-.476	48.621	1.00	24.10	A
ATOM	2283	CG1	VAL	A	291	.206	.154	49.883	1.00	25.41	A
ATOM	2284	CG2	VAL	A	291	-.301	.523	47.470	1.00	27.46	A
ATOM	2285	C	VAL	A	291	.612	-2.654	49.463	1.00	20.08	A
ATOM	2286	O	VAL	A	291	1.705	-2.749	50.011	1.00	22.04	A
ATOM	2287	N	LYS	A	292	-.457	-3.325	49.882	1.00	22.59	A
ATOM	2288	CA	LYS	A	292	-.370	-4.204	51.046	1.00	27.62	A
ATOM	2289	CB	LYS	A	292	-1.719	-4.865	51.343	1.00	27.32	A
ATOM	2290	CG	LYS	A	292	-2.807	-3.876	51.724	1.00	34.18	A
ATOM	2291	CD	LYS	A	292	-4.056	-4.574	52.247	1.00	36.81	A
ATOM	2292	CE	LYS	A	292	-3.813	-5.218	53.602	1.00	39.97	A
ATOM	2293	NZ	LYS	A	292	-5.034	-5.931	54.086	1.00	46.52	A
ATOM	2294	C	LYS	A	292	.694	-5.282	50.908	1.00	25.15	A
ATOM	2295	O	LYS	A	292	1.351	-5.630	51.888	1.00	27.45	A
ATOM	2296	N	GLN	A	293	.891	-5.790	49.697	1.00	24.58	A
ATOM	2297	CA	GLN	A	293	1.880	-6.843	49.491	1.00	23.75	A
ATOM	2298	CB	GLN	A	293	1.449	-7.750	48.336	1.00	27.81	A
ATOM	2299	CG	GLN	A	293	.218	-8.584	48.612	1.00	37.43	A
ATOM	2300	CD	GLN	A	293	-.083	-9.552	47.491	1.00	37.04	A
ATOM	2301	OE1	GLN	A	293	-.975	-10.374	47.603	1.00	46.50	A
ATOM	2302	NE2	GLN	A	293	.661	-9.453	46.400	1.00	51.17	A
ATOM	2303	C	GLN	A	293	3.305	-6.381	49.222	1.00	27.18	A
ATOM	2304	O	GLN	A	293	4.252	-7.122	49.493	1.00	21.63	A
ATOM	2305	N	ASN	A	294	3.468	-5.169	48.698	1.00	23.16	A
ATOM	2306	CA	ASN	A	294	4.802	-4.692	48.353	1.00	22.58	A
ATOM	2307	CB	ASN	A	294	4.856	-4.419	46.849	1.00	17.92	A
ATOM	2308	CG	ASN	A	294	4.603	-5.672	46.018	1.00	25.52	A
ATOM	2309	OD1	ASN	A	294	5.480	-6.523	45.871	1.00	28.01	A
ATOM	2310	ND2	ASN	A	294	3.398	-5.792	45.478	1.00	21.76	A
ATOM	2311	C	ASN	A	294	5.370	-3.489	49.116	1.00	25.67	A
ATOM	2312	O	ASN	A	294	6.514	-3.114	48.898	1.00	26.19	A
ATOM	2313	N	ALA	A	295	4.589	-2.882	50.002	1.00	27.22	A
ATOM	2314	CA	ALA	A	295	5.097	-1.747	50.775	1.00	28.74	A
ATOM	2315	CB	ALA	A	295	3.969	-.751	51.060	1.00	26.02	A
ATOM	2316	C	ALA	A	295	5.717	-2.224	52.093	1.00	29.23	A
ATOM	2317	O	ALA	A	295	5.469	-3.346	52.533	1.00	29.95	A
ATOM	2318	N	GLY	A	296	6.520	-1.370	52.721	1.00	29.14	A
ATOM	2319	CA	GLY	A	296	7.128	-1.740	53.986	1.00	29.13	A
ATOM	2320	C	GLY	A	296	8.505	-2.363	53.854	1.00	32.07	A
ATOM	2321	O	GLY	A	296	9.089	-2.383	52.765	1.00	29.59	A
ATOM	2322	N	VAL	A	297	9.013	-2.890	54.968	1.00	33.38	A
ATOM	2323	CA	VAL	A	297	10.344	-3.490	55.004	1.00	32.44	A
ATOM	2324	CB	VAL	A	297	10.955	-3.398	56.414	1.00	29.28	A
ATOM	2325	CG1	VAL	A	297	10.925	-1.952	56.898	1.00	28.64	A
ATOM	2326	CG2	VAL	A	297	10.198	-4.294	57.369	1.00	32.71	A
ATOM	2327	C	VAL	A	297	10.350	-4.946	54.568	1.00	33.21	A
ATOM	2328	O	VAL	A	297	9.321	-5.621	54.609	1.00	32.57	A
ATOM	2329	N	GLY	A	298	11.518	-5.413	54.139	1.00	31.43	A
ATOM	2330	CA	GLY	A	298	11.658	-6.784	53.700	1.00	34.45	A
ATOM	2331	C	GLY	A	298	11.136	-7.093	52.309	1.00	35.52	A
ATOM	2332	O	GLY	A	298	11.112	-8.255	51.912	1.00	38.05	A
ATOM	2333	N	LYS	A	299	10.728	-6.077	51.558	1.00	36.66	A
ATOM	2334	CA	LYS	A	299	10.197	-6.307	50.213	1.00	35.41	A

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ATOM   2335  CB  LYS A 299       9.007  -5.383  49.958  1.00 35.48      A
ATOM   2336  CG  LYS A 299       7.892  -5.516  50.979  1.00 34.51      A
ATOM   2337  CD  LYS A 299       7.424  -6.962  51.114  1.00 34.42      A
ATOM   2338  CE  LYS A 299       6.209  -7.055  52.021  1.00 38.24      A
ATOM   2339  NZ  LYS A 299       6.459  -6.394  53.330  1.00 41.55      A
ATOM   2340  C   LYS A 299      11.239  -6.137  49.106  1.00 38.29      A
ATOM   2341  O   LYS A 299      11.083  -6.656  48.008  1.00 41.19      A
ATOM   2342  N   ILE A 300      12.317  -5.428  49.385  1.00 41.07      A
ATOM   2343  CA  ILE A 300      13.340  -5.244  48.373  1.00 44.23      A
ATOM   2344  CB  ILE A 300      13.212  -3.876  47.676  1.00 41.18      A
ATOM   2345  CG2 ILE A 300      12.064  -3.914  46.696  1.00 44.16      A
ATOM   2346  CG1 ILE A 300      13.001  -2.763  48.709  1.00 38.69      A
ATOM   2347  CD1 ILE A 300      14.252  -2.341  49.428  1.00 31.92      A
ATOM   2348  C   ILE A 300      14.695  -5.343  49.010  1.00 48.79      A
ATOM   2349  O   ILE A 300      14.821  -5.258  50.228  1.00 51.43      A
ATOM   2350  N   ASN A 301      15.710  -5.526  48.184  1.00 53.37      A
ATOM   2351  CA  ASN A 301      17.080  -5.629  48.662  1.00 57.57      A
ATOM   2352  CB  ASN A 301      17.741  -6.897  48.104  1.00 63.65      A
ATOM   2353  CG  ASN A 301      17.080  -8.162  48.611  1.00 68.12      A
ATOM   2354  OD1 ASN A 301      16.118  -8.671  48.015  1.00 71.42      A
ATOM   2355  ND2 ASN A 301      17.575  -8.668  49.736  1.00 71.08      A
ATOM   2356  C   ASN A 301      17.831  -4.397  48.190  1.00 57.52      A
ATOM   2357  O   ASN A 301      18.342  -4.363  47.073  1.00 57.52      A
ATOM   2358  N   PRO A 302      17.891  -3.357  49.037  1.00 57.49      A
ATOM   2359  CD  PRO A 302      17.343  -3.297  50.406  1.00 57.08      A
ATOM   2360  CA  PRO A 302      18.585  -2.115  48.690  1.00 57.89      A
ATOM   2361  CB  PRO A 302      18.271  -1.208  49.875  1.00 58.22      A
ATOM   2362  CG  PRO A 302      18.160  -2.199  51.026  1.00 58.64      A
ATOM   2363  C   PRO A 302      20.080  -2.332  48.502  1.00 60.23      A
ATOM   2364  O   PRO A 302      20.535  -3.481  48.750  1.00 61.47      A
ATOM   2365  OXT PRO A 302      20.773  -1.357  48.117  1.00 57.60      A
ATOM   2366  CB  ALA B   1      13.653  -9.176  22.684  1.00 29.27      B
ATOM   2367  C   ALA B   1      12.117  -8.632  24.574  1.00 25.78      B
ATOM   2368  O   ALA B   1      10.944  -8.257  24.512  1.00 26.48      B
ATOM   2369  N   ALA B   1      11.519 -10.375  22.923  1.00 31.71      B
ATOM   2370  CA  ALA B   1      12.637  -9.742  23.666  1.00 26.69      B
ATOM   2371  N   ASP B   2      13.008  -8.104  25.406  1.00 27.91      B
ATOM   2372  CA  ASP B   2      12.672  -7.040  26.353  1.00 28.12      B
ATOM   2373  CB  ASP B   2      13.831  -6.873  27.343  1.00 29.77      B
ATOM   2374  CG  ASP B   2      13.523  -5.889  28.447  1.00 32.29      B
ATOM   2375  OD1 ASP B   2      12.448  -5.251  28.414  1.00 34.65      B
ATOM   2376  OD2 ASP B   2      14.366  -5.752  29.354  1.00 40.92      B
ATOM   2377  C   ASP B   2      12.404  -5.714  25.630  1.00 27.48      B
ATOM   2378  O   ASP B   2      13.331  -5.100  25.110  1.00 27.69      B
ATOM   2379  N   PHE B   3      11.140  -5.284  25.603  1.00 24.35      B
ATOM   2380  CA  PHE B   3      10.741  -4.037  24.928  1.00 26.87      B
ATOM   2381  CB  PHE B   3       9.453  -4.239  24.115  1.00 22.20      B
ATOM   2382  CG  PHE B   3       9.632  -5.015  22.833  1.00 25.87      B
ATOM   2383  CD1 PHE B   3       8.515  -5.399  22.090  1.00 24.86      B
ATOM   2384  CD2 PHE B   3      10.897  -5.358  22.363  1.00 26.09      B
ATOM   2385  CE1 PHE B   3       8.654  -6.113  20.901  1.00 28.14      B
ATOM   2386  CE2 PHE B   3      11.046  -6.070  21.173  1.00 24.37      B
ATOM   2387  CZ  PHE B   3       9.920  -6.448  20.443  1.00 29.34      B
ATOM   2388  C   PHE B   3      10.506  -2.859  25.873  1.00 27.48      B
ATOM   2389  O   PHE B   3       9.951  -1.836  25.467  1.00 24.70      B
ATOM   2390  N   SER B   4      10.909  -2.995  27.130  1.00 24.49      B
ATOM   2391  CA  SER B   4      10.699  -1.911  28.078  1.00 23.42      B
ATOM   2392  CB  SER B   4      10.900  -2.404  29.513  1.00 24.87      B
ATOM   2393  OG  SER B   4      12.216  -2.883  29.705  1.00 31.37      B
ATOM   2394  C   SER B   4      11.649   -.751  27.790  1.00 25.88      B
ATOM   2395  O   SER B   4      12.651   -.913  27.104  1.00 27.65      B
ATOM   2396  N   LEU B   5      11.321    .416  28.329  1.00 22.89      B
ATOM   2397  CA  LEU B   5      12.119   1.619  28.137  1.00 25.22      B
ATOM   2398  CB  LEU B   5      11.383   2.833  28.707  1.00 21.85      B
ATOM   2399  CG  LEU B   5      12.108   4.183  28.644  1.00 25.91      B
ATOM   2400  CD1 LEU B   5      12.363   4.575  27.201  1.00 22.72      B
ATOM   2401  CD2 LEU B   5      11.264   5.242  29.340  1.00 23.82      B
ATOM   2402  C   LEU B   5      13.493   1.535  28.782  1.00 27.51      B
ATOM   2403  O   LEU B   5      13.623   1.201  29.958  1.00 25.18      B
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ATOM	2404	N	LYS	B	6	14.517	1.844	27.998	1.00	25.97	B
ATOM	2405	CA	LYS	B	6	15.894	1.843	28.479	1.00	24.16	B
ATOM	2406	CB	LYS	B	6	16.708	.721	27.829	1.00	23.30	B
ATOM	2407	CG	LYS	B	6	16.101	-.659	27.897	1.00	30.69	B
ATOM	2408	CD	LYS	B	6	16.077	-1.205	29.317	1.00	30.47	B
ATOM	2409	CE	LYS	B	6	15.627	-2.664	29.316	1.00	34.53	B
ATOM	2410	NZ	LYS	B	6	15.532	-3.218	30.701	1.00	39.68	B
ATOM	2411	C	LYS	B	6	16.526	3.169	28.070	1.00	27.01	B
ATOM	2412	O	LYS	B	6	16.027	3.847	27.176	1.00	27.44	B
ATOM	2413	N	GLY	B	7	17.616	3.537	28.734	1.00	26.98	B
ATOM	2414	CA	GLY	B	7	18.324	4.747	28.374	1.00	23.03	B
ATOM	2415	C	GLY	B	7	17.906	6.080	28.936	1.00	26.38	B
ATOM	2416	O	GLY	B	7	17.134	6.173	29.887	1.00	26.53	B
ATOM	2417	N	PHE	B	8	18.434	7.127	28.309	1.00	25.01	B
ATOM	2418	CA	PHE	B	8	18.194	8.504	28.712	1.00	25.77	B
ATOM	2419	CB	PHE	B	8	18.901	9.456	27.753	1.00	26.18	B
ATOM	2420	CG	PHE	B	8	20.389	9.555	27.979	1.00	32.39	B
ATOM	2421	CD1	PHE	B	8	21.285	9.092	27.016	1.00	31.68	B
ATOM	2422	CD2	PHE	B	8	20.891	10.136	29.138	1.00	30.80	B
ATOM	2423	CE1	PHE	B	8	22.664	9.210	27.202	1.00	33.73	B
ATOM	2424	CE2	PHE	B	8	22.266	10.261	29.339	1.00	34.97	B
ATOM	2425	CZ	PHE	B	8	23.158	9.794	28.360	1.00	33.55	B
ATOM	2426	C	PHE	B	8	16.754	8.966	28.884	1.00	22.39	B
ATOM	2427	O	PHE	B	8	16.499	9.866	29.689	1.00	26.18	B
ATOM	2428	N	ALA	B	9	15.820	8.384	28.138	1.00	19.15	B
ATOM	2429	CA	ALA	B	9	14.419	8.784	28.260	1.00	22.48	B
ATOM	2430	CB	ALA	B	9	13.630	8.329	27.033	1.00	19.89	B
ATOM	2431	C	ALA	B	9	13.789	8.222	29.540	1.00	21.56	B
ATOM	2432	O	ALA	B	9	12.699	8.623	29.936	1.00	24.72	B
ATOM	2433	N	ALA	B	10	14.489	7.295	30.185	1.00	25.79	B
ATOM	2434	CA	ALA	B	10	13.999	6.693	31.418	1.00	29.06	B
ATOM	2435	CB	ALA	B	10	14.567	5.286	31.579	1.00	29.20	B
ATOM	2436	C	ALA	B	10	14.389	7.558	32.614	1.00	32.27	B
ATOM	2437	O	ALA	B	10	13.940	7.331	33.731	1.00	34.41	B
ATOM	2438	N	LEU	B	11	15.226	8.561	32.368	1.00	31.08	B
ATOM	2439	CA	LEU	B	11	15.674	9.465	33.422	1.00	30.59	B
ATOM	2440	CB	LEU	B	11	17.131	9.868	33.191	1.00	27.81	B
ATOM	2441	CG	LEU	B	11	18.151	8.730	33.191	1.00	34.60	B
ATOM	2442	CD1	LEU	B	11	19.527	9.303	32.966	1.00	36.55	B
ATOM	2443	CD2	LEU	B	11	18.096	7.978	34.518	1.00	39.49	B
ATOM	2444	C	LEU	B	11	14.826	10.728	33.499	1.00	31.22	B
ATOM	2445	O	LEU	B	11	13.882	10.907	32.720	1.00	27.54	B
ATOM	2446	N	ASN	B	12	15.180	11.606	34.438	1.00	25.29	B
ATOM	2447	CA	ASN	B	12	14.478	12.867	34.638	1.00	26.29	B
ATOM	2448	CB	ASN	B	12	14.816	13.814	33.481	1.00	30.82	B
ATOM	2449	CG	ASN	B	12	14.330	15.236	33.714	1.00	34.67	B
ATOM	2450	OD1	ASN	B	12	14.782	15.921	34.639	1.00	38.14	B
ATOM	2451	ND2	ASN	B	12	13.407	15.693	32.864	1.00	34.99	B
ATOM	2452	C	ASN	B	12	12.954	12.659	34.749	1.00	27.65	B
ATOM	2453	O	ASN	B	12	12.172	13.489	34.274	1.00	25.74	B
ATOM	2454	N	GLY	B	13	12.541	11.550	35.369	1.00	24.27	B
ATOM	2455	CA	GLY	B	13	11.123	11.269	35.534	1.00	31.13	B
ATOM	2456	C	GLY	B	13	10.558	10.173	34.644	1.00	29.22	B
ATOM	2457	O	GLY	B	13	9.443	9.704	34.863	1.00	30.17	B
ATOM	2458	N	GLY	B	14	11.322	9.771	33.634	1.00	28.63	B
ATOM	2459	CA	GLY	B	14	10.864	8.726	32.743	1.00	26.09	B
ATOM	2460	C	GLY	B	14	9.978	9.237	31.621	1.00	25.46	B
ATOM	2461	O	GLY	B	14	9.678	10.427	31.530	1.00	21.24	B
ATOM	2462	N	THR	B	15	9.558	8.324	30.757	1.00	24.22	B
ATOM	2463	CA	THR	B	15	8.706	8.685	29.640	1.00	21.22	B
ATOM	2464	CB	THR	B	15	9.503	8.673	28.318	1.00	19.62	B
ATOM	2465	OG1	THR	B	15	10.581	9.613	28.400	1.00	20.23	B
ATOM	2466	CG2	THR	B	15	8.604	9.032	27.149	1.00	22.44	B
ATOM	2467	C	THR	B	15	7.544	7.706	29.537	1.00	21.56	B
ATOM	2468	O	THR	B	15	7.747	6.510	29.341	1.00	24.87	B
ATOM	2469	N	THR	B	16	6.327	8.218	29.672	1.00	20.15	B
ATOM	2470	CA	THR	B	16	5.141	7.379	29.579	1.00	21.93	B
ATOM	2471	CB	THR	B	16	4.352	7.386	30.896	1.00	22.48	B
ATOM	2472	OG1	THR	B	16	3.885	8.714	31.169	1.00	22.97	B

ATOM	2473	CG2	THR	B	16	5.239	6.909	32.040	1.00	24.84	B
ATOM	2474	C	THR	B	16	4.233	7.863	28.457	1.00	22.31	B
ATOM	2475	O	THR	B	16	3.198	7.266	28.185	1.00	24.29	B
ATOM	2476	N	GLY	B	17	4.623	8.955	27.813	1.00	20.58	B
ATOM	2477	CA	GLY	B	17	3.820	9.480	26.727	1.00	24.74	B
ATOM	2478	C	GLY	B	17	2.380	9.776	27.107	1.00	22.36	B
ATOM	2479	O	GLY	B	17	2.118	10.399	28.132	1.00	23.49	B
ATOM	2480	N	GLY	B	18	1.445	9.320	26.279	1.00	24.56	B
ATOM	2481	CA	GLY	B	18	.038	9.583	26.537	1.00	26.88	B
ATOM	2482	C	GLY	B	18	-.717	8.450	27.193	1.00	30.11	B
ATOM	2483	O	GLY	B	18	-1.945	8.422	27.153	1.00	27.22	B
ATOM	2484	N	GLU	B	19	.017	7.506	27.781	1.00	30.44	B
ATOM	2485	CA	GLU	B	19	-.590	6.369	28.480	1.00	38.96	B
ATOM	2486	CB	GLU	B	19	.496	5.360	28.854	1.00	38.43	B
ATOM	2487	CG	GLU	B	19	1.100	4.679	27.645	1.00	46.43	B
ATOM	2488	CD	GLU	B	19	.054	3.905	26.862	1.00	52.16	B
ATOM	2489	OE1	GLU	B	19	.280	3.613	25.662	1.00	52.68	B
ATOM	2490	OE2	GLU	B	19	-1.002	3.580	27.457	1.00	57.24	B
ATOM	2491	C	GLU	B	19	-1.326	6.832	29.739	1.00	38.13	B
ATOM	2492	O	GLU	B	19	-.836	7.700	30.468	1.00	42.40	B
ATOM	2493	N	GLY	B	20	-2.509	6.274	29.982	1.00	43.17	B
ATOM	2494	CA	GLY	B	20	-3.281	6.646	31.164	1.00	46.24	B
ATOM	2495	C	GLY	B	20	-4.223	7.829	31.010	1.00	46.66	B
ATOM	2496	O	GLY	B	20	-4.634	8.431	32.009	1.00	48.27	B
ATOM	2497	N	GLY	B	21	-4.561	8.171	29.768	1.00	44.33	B
ATOM	2498	CA	GLY	B	21	-5.460	9.285	29.515	1.00	42.49	B
ATOM	2499	C	GLY	B	21	-6.510	8.962	28.463	1.00	41.18	B
ATOM	2500	O	GLY	B	21	-7.015	7.843	28.408	1.00	37.26	B
ATOM	2501	N	GLN	B	22	-6.847	9.939	27.628	1.00	38.70	B
ATOM	2502	CA	GLN	B	22	-7.836	9.728	26.579	1.00	35.73	B
ATOM	2503	CB	GLN	B	22	-8.401	11.056	26.083	1.00	39.61	B
ATOM	2504	CG	GLN	B	22	-9.066	11.928	27.132	1.00	53.41	B
ATOM	2505	CD	GLN	B	22	-9.548	13.243	26.528	1.00	60.64	B
ATOM	2506	OE1	GLN	B	22	-8.863	13.842	25.684	1.00	63.02	B
ATOM	2507	NE2	GLN	B	22	-10.721	13.705	26.962	1.00	65.84	B
ATOM	2508	C	GLN	B	22	-7.214	9.010	25.385	1.00	35.50	B
ATOM	2509	O	GLN	B	22	-5.995	9.033	25.180	1.00	30.90	B
ATOM	2510	N	THR	B	23	-8.071	8.396	24.584	1.00	30.40	B
ATOM	2511	CA	THR	B	23	-7.623	7.671	23.415	1.00	35.00	B
ATOM	2512	CB	THR	B	23	-7.766	6.160	23.629	1.00	36.03	B
ATOM	2513	OG1	THR	B	23	-6.908	5.749	24.704	1.00	41.76	B
ATOM	2514	CG2	THR	B	23	-7.390	5.407	22.368	1.00	39.64	B
ATOM	2515	C	THR	B	23	-8.442	8.069	22.198	1.00	36.18	B
ATOM	2516	O	THR	B	23	-9.669	8.139	22.261	1.00	35.80	B
ATOM	2517	N	VAL	B	24	-7.759	8.338	21.094	1.00	34.47	B
ATOM	2518	CA	VAL	B	24	-8.430	8.704	19.856	1.00	34.49	B
ATOM	2519	CB	VAL	B	24	-8.292	10.209	19.553	1.00	37.18	B
ATOM	2520	CG1	VAL	B	24	-9.200	10.585	18.390	1.00	41.11	B
ATOM	2521	CG2	VAL	B	24	-8.636	11.024	20.787	1.00	40.34	B
ATOM	2522	C	VAL	B	24	-7.807	7.929	18.703	1.00	32.12	B
ATOM	2523	O	VAL	B	24	-6.629	7.572	18.747	1.00	27.68	B
ATOM	2524	N	THR	B	25	-8.610	7.653	17.683	1.00	28.47	B
ATOM	2525	CA	THR	B	25	-8.128	6.939	16.511	1.00	33.41	B
ATOM	2526	CB	THR	B	25	-8.898	5.626	16.290	1.00	34.21	B
ATOM	2527	OG1	THR	B	25	-8.755	4.783	17.442	1.00	37.71	B
ATOM	2528	CG2	THR	B	25	-8.359	4.899	15.061	1.00	35.20	B
ATOM	2529	C	THR	B	25	-8.354	7.860	15.316	1.00	36.74	B
ATOM	2530	O	THR	B	25	-9.450	8.407	15.147	1.00	32.59	B
ATOM	2531	N	VAL	B	26	-7.321	8.034	14.496	1.00	31.14	B
ATOM	2532	CA	VAL	B	26	-7.420	8.909	13.337	1.00	31.46	B
ATOM	2533	CB	VAL	B	26	-6.485	10.128	13.477	1.00	30.20	B
ATOM	2534	CG1	VAL	B	26	-6.823	10.911	14.741	1.00	29.96	B
ATOM	2535	CG2	VAL	B	26	-5.038	9.668	13.508	1.00	27.31	B
ATOM	2536	C	VAL	B	26	-7.055	8.167	12.063	1.00	32.55	B
ATOM	2537	O	VAL	B	26	-6.401	7.131	12.107	1.00	32.22	B
ATOM	2538	N	THR	B	27	-7.479	8.705	10.926	1.00	31.75	B
ATOM	2539	CA	THR	B	27	-7.190	8.083	9.642	1.00	35.07	B
ATOM	2540	CB	THR	B	27	-8.453	7.428	9.041	1.00	32.85	B
ATOM	2541	OG1	THR	B	27	-9.448	8.432	8.802	1.00	33.22	B

ATOM	2542	CG2	THR	B	27	-9.020	6.395	10.005	1.00	38.75	B
ATOM	2543	C	THR	B	27	-6.631	9.087	8.641	1.00	33.12	B
ATOM	2544	O	THR	B	27	-6.259	8.717	7.531	1.00	36.13	B
ATOM	2545	N	THR	B	28	-6.561	10.355	9.030	1.00	33.02	B
ATOM	2546	CA	THR	B	28	-6.032	11.379	8.133	1.00	28.84	B
ATOM	2547	CB	THR	B	28	-7.152	12.218	7.499	1.00	31.41	B
ATOM	2548	OG1	THR	B	28	-7.750	13.042	8.510	1.00	28.60	B
ATOM	2549	CG2	THR	B	28	-8.218	11.322	6.881	1.00	27.96	B
ATOM	2550	C	THR	B	28	-5.133	12.337	8.883	1.00	30.80	B
ATOM	2551	O	THR	B	28	-5.206	12.440	10.106	1.00	31.08	B
ATOM	2552	N	GLY	B	29	-4.287	13.047	8.143	1.00	30.82	B
ATOM	2553	CA	GLY	B	29	-3.403	14.010	8.767	1.00	30.58	B
ATOM	2554	C	GLY	B	29	-4.195	15.100	9.463	1.00	32.12	B
ATOM	2555	O	GLY	B	29	-3.843	15.531	10.564	1.00	27.80	B
ATOM	2556	N	ASP	B	30	-5.274	15.546	8.823	1.00	30.49	B
ATOM	2557	CA	ASP	B	30	-6.108	16.601	9.384	1.00	32.58	B
ATOM	2558	CB	ASP	B	30	-7.150	17.056	8.356	1.00	32.57	B
ATOM	2559	CG	ASP	B	30	-6.570	18.027	7.322	1.00	39.67	B
ATOM	2560	OD1	ASP	B	30	-7.225	18.267	6.284	1.00	38.49	B
ATOM	2561	OD2	ASP	B	30	-5.466	18.560	7.555	1.00	34.94	B
ATOM	2562	C	ASP	B	30	-6.786	16.198	10.692	1.00	32.12	B
ATOM	2563	O	ASP	B	30	-6.953	17.031	11.584	1.00	34.52	B
ATOM	2564	N	GLN	B	31	-7.175	14.933	10.818	1.00	30.26	B
ATOM	2565	CA	GLN	B	31	-7.798	14.482	12.057	1.00	30.55	B
ATOM	2566	CB	GLN	B	31	-8.418	13.097	11.886	1.00	31.17	B
ATOM	2567	CG	GLN	B	31	-9.436	13.020	10.763	1.00	37.62	B
ATOM	2568	CD	GLN	B	31	-10.124	11.668	10.688	1.00	39.96	B
ATOM	2569	OE1	GLN	B	31	-9.579	10.653	11.112	1.00	39.36	B
ATOM	2570	NE2	GLN	B	31	-11.327	11.651	10.132	1.00	42.83	B
ATOM	2571	C	GLN	B	31	-6.722	14.438	13.141	1.00	28.76	B
ATOM	2572	O	GLN	B	31	-6.971	14.809	14.290	1.00	29.49	B
ATOM	2573	N	LEU	B	32	-5.526	13.990	12.767	1.00	24.87	B
ATOM	2574	CA	LEU	B	32	-4.412	13.914	13.707	1.00	27.72	B
ATOM	2575	CB	LEU	B	32	-3.205	13.264	13.018	1.00	25.09	B
ATOM	2576	CG	LEU	B	32	-1.856	13.129	13.725	1.00	32.02	B
ATOM	2577	CD1	LEU	B	32	-2.027	12.635	15.142	1.00	32.05	B
ATOM	2578	CD2	LEU	B	32	-.987	12.182	12.928	1.00	28.03	B
ATOM	2579	C	LEU	B	32	-4.079	15.324	14.227	1.00	30.68	B
ATOM	2580	O	LEU	B	32	-3.974	15.545	15.434	1.00	28.27	B
ATOM	2581	N	ILE	B	33	-3.943	16.285	13.321	1.00	32.26	B
ATOM	2582	CA	ILE	B	33	-3.658	17.658	13.723	1.00	31.80	B
ATOM	2583	CB	ILE	B	33	-3.526	18.567	12.482	1.00	35.71	B
ATOM	2584	CG2	ILE	B	33	-3.543	20.032	12.888	1.00	35.77	B
ATOM	2585	CG1	ILE	B	33	-2.237	18.213	11.739	1.00	34.57	B
ATOM	2586	CD1	ILE	B	33	-2.057	18.942	10.437	1.00	40.23	B
ATOM	2587	C	ILE	B	33	-4.763	18.185	14.649	1.00	32.74	B
ATOM	2588	O	ILE	B	33	-4.486	18.840	15.653	1.00	29.85	B
ATOM	2589	N	ALA	B	34	-6.013	17.875	14.315	1.00	29.59	B
ATOM	2590	CA	ALA	B	34	-7.160	18.301	15.116	1.00	29.57	B
ATOM	2591	CB	ALA	B	34	-8.456	17.853	14.437	1.00	29.81	B
ATOM	2592	C	ALA	B	34	-7.094	17.732	16.542	1.00	32.54	B
ATOM	2593	O	ALA	B	34	-7.345	18.441	17.518	1.00	28.57	B
ATOM	2594	N	ALA	B	35	-6.756	16.451	16.656	1.00	29.50	B
ATOM	2595	CA	ALA	B	35	-6.669	15.800	17.962	1.00	29.65	B
ATOM	2596	CB	ALA	B	35	-6.378	14.305	17.790	1.00	24.41	B
ATOM	2597	C	ALA	B	35	-5.595	16.453	18.832	1.00	30.58	B
ATOM	2598	O	ALA	B	35	-5.776	16.610	20.038	1.00	29.82	B
ATOM	2599	N	LEU	B	36	-4.478	16.833	18.225	1.00	27.20	B
ATOM	2600	CA	LEU	B	36	-3.404	17.470	18.978	1.00	27.84	B
ATOM	2601	CB	LEU	B	36	-2.129	17.543	18.134	1.00	25.38	B
ATOM	2602	CG	LEU	B	36	-1.400	16.216	17.889	1.00	29.08	B
ATOM	2603	CD1	LEU	B	36	-.238	16.421	16.927	1.00	28.60	B
ATOM	2604	CD2	LEU	B	36	-.896	15.665	19.207	1.00	28.20	B
ATOM	2605	C	LEU	B	36	-3.794	18.874	19.424	1.00	34.25	B
ATOM	2606	O	LEU	B	36	-3.458	19.306	20.532	1.00	34.36	B
ATOM	2607	N	LYS	B	37	-4.499	19.584	18.553	1.00	33.34	B
ATOM	2608	CA	LYS	B	37	-4.917	20.943	18.845	1.00	37.03	B
ATOM	2609	CB	LYS	B	37	-5.506	21.597	17.594	1.00	41.61	B
ATOM	2610	CG	LYS	B	37	-4.476	21.887	16.534	1.00	45.83	B

ATOM	2611	CD	LYS	B	37	-4.957	22.964	15.569	1.00	53.97	B
ATOM	2612	CE	LYS	B	37	-3.756	23.723	15.022	1.00	59.51	B
ATOM	2613	NZ	LYS	B	37	-2.860	24.177	16.154	1.00	62.25	B
ATOM	2614	C	LYS	B	37	-5.921	21.036	19.969	1.00	36.80	B
ATOM	2615	O	LYS	B	37	-5.879	21.970	20.760	1.00	37.38	B
ATOM	2616	N	ASN	B	38	-6.826	20.067	20.035	1.00	38.51	B
ATOM	2617	CA	ASN	B	38	-7.864	20.057	21.061	1.00	39.09	B
ATOM	2618	CB	ASN	B	38	-9.169	19.534	20.464	1.00	42.52	B
ATOM	2619	CG	ASN	B	38	-9.656	20.378	19.312	1.00	45.71	B
ATOM	2620	OD1	ASN	B	38	-9.896	21.580	19.469	1.00	47.44	B
ATOM	2621	ND2	ASN	B	38	-9.803	19.761	18.140	1.00	44.39	B
ATOM	2622	C	ASN	B	38	-7.515	19.235	22.302	1.00	39.14	B
ATOM	2623	O	ASN	B	38	-8.397	18.872	23.084	1.00	38.44	B
ATOM	2624	N	LYS	B	39	-6.239	18.925	22.479	1.00	37.43	B
ATOM	2625	CA	LYS	B	39	-5.818	18.158	23.648	1.00	36.31	B
ATOM	2626	CB	LYS	B	39	-4.339	17.788	23.562	1.00	33.59	B
ATOM	2627	CG	LYS	B	39	-3.859	17.062	24.806	1.00	36.26	B
ATOM	2628	CD	LYS	B	39	-2.382	16.766	24.784	1.00	33.85	B
ATOM	2629	CE	LYS	B	39	-1.967	16.023	26.052	1.00	35.35	B
ATOM	2630	NZ	LYS	B	39	-2.168	16.840	27.279	1.00	32.68	B
ATOM	2631	C	LYS	B	39	-6.021	18.929	24.937	1.00	32.91	B
ATOM	2632	O	LYS	B	39	-5.687	20.107	25.020	1.00	33.83	B
ATOM	2633	N	ASN	B	40	-6.575	18.260	25.939	1.00	35.09	B
ATOM	2634	CA	ASN	B	40	-6.754	18.882	27.242	1.00	37.25	B
ATOM	2635	CB	ASN	B	40	-7.738	18.085	28.096	1.00	43.17	B
ATOM	2636	CG	ASN	B	40	-7.979	18.730	29.444	1.00	52.17	B
ATOM	2637	OD1	ASN	B	40	-7.033	18.994	30.198	1.00	56.38	B
ATOM	2638	ND2	ASN	B	40	-9.248	18.990	29.763	1.00	58.36	B
ATOM	2639	C	ASN	B	40	-5.363	18.833	27.883	1.00	35.69	B
ATOM	2640	O	ASN	B	40	-4.758	17.765	27.986	1.00	32.45	B
ATOM	2641	N	ALA	B	41	-4.858	19.991	28.294	1.00	35.70	B
ATOM	2642	CA	ALA	B	41	-3.532	20.083	28.897	1.00	40.13	B
ATOM	2643	CB	ALA	B	41	-3.215	21.536	29.207	1.00	41.22	B
ATOM	2644	C	ALA	B	41	-3.357	19.246	30.156	1.00	39.85	B
ATOM	2645	O	ALA	B	41	-2.239	18.914	30.547	1.00	39.61	B
ATOM	2646	N	ASN	B	42	-4.469	18.883	30.778	1.00	40.47	B
ATOM	2647	CA	ASN	B	42	-4.435	18.131	32.022	1.00	45.70	B
ATOM	2648	CB	ASN	B	42	-5.505	18.687	32.948	1.00	51.85	B
ATOM	2649	CG	ASN	B	42	-5.165	20.063	33.419	1.00	57.07	B
ATOM	2650	OD1	ASN	B	42	-4.445	20.225	34.398	1.00	71.51	B
ATOM	2651	ND2	ASN	B	42	-5.638	21.068	32.707	1.00	61.11	B
ATOM	2652	C	ASN	B	42	-4.624	16.644	31.878	1.00	45.41	B
ATOM	2653	O	ASN	B	42	-4.616	15.915	32.867	1.00	45.10	B
ATOM	2654	N	THR	B	43	-4.796	16.193	30.646	1.00	40.05	B
ATOM	2655	CA	THR	B	43	-5.015	14.786	30.403	1.00	39.96	B
ATOM	2656	CB	THR	B	43	-6.478	14.541	29.982	1.00	42.54	B
ATOM	2657	OG1	THR	B	43	-7.343	14.891	31.068	1.00	49.18	B
ATOM	2658	CG2	THR	B	43	-6.704	13.083	29.614	1.00	48.03	B
ATOM	2659	C	THR	B	43	-4.088	14.243	29.330	1.00	36.25	B
ATOM	2660	O	THR	B	43	-3.912	14.856	28.278	1.00	35.12	B
ATOM	2661	N	PRO	B	44	-3.445	13.100	29.610	1.00	33.79	B
ATOM	2662	CD	PRO	B	44	-3.380	12.433	30.921	1.00	35.20	B
ATOM	2663	CA	PRO	B	44	-2.535	12.463	28.659	1.00	31.80	B
ATOM	2664	CB	PRO	B	44	-2.035	11.243	29.426	1.00	31.73	B
ATOM	2665	CG	PRO	B	44	-2.048	11.724	30.847	1.00	31.86	B
ATOM	2666	C	PRO	B	44	-3.376	12.067	27.449	1.00	32.35	B
ATOM	2667	O	PRO	B	44	-4.552	11.724	27.593	1.00	27.82	B
ATOM	2668	N	LEU	B	45	-2.787	12.116	26.261	1.00	27.90	B
ATOM	2669	CA	LEU	B	45	-3.531	11.757	25.058	1.00	26.85	B
ATOM	2670	CB	LEU	B	45	-3.761	13.002	24.189	1.00	24.30	B
ATOM	2671	CG	LEU	B	45	-4.459	12.771	22.848	1.00	25.02	B
ATOM	2672	CD1	LEU	B	45	-5.891	12.334	23.081	1.00	27.36	B
ATOM	2673	CD2	LEU	B	45	-4.409	14.044	22.019	1.00	25.57	B
ATOM	2674	C	LEU	B	45	-2.801	10.682	24.254	1.00	25.38	B
ATOM	2675	O	LEU	B	45	-1.605	10.794	23.991	1.00	22.44	B
ATOM	2676	N	LYS	B	46	-3.528	9.633	23.892	1.00	21.15	B
ATOM	2677	CA	LYS	B	46	-2.970	8.543	23.108	1.00	25.24	B
ATOM	2678	CB	LYS	B	46	-3.131	7.209	23.836	1.00	27.39	B
ATOM	2679	CG	LYS	B	46	-2.483	6.033	23.124	1.00	33.79	B

ATOM	2680	CD	LYS	B	46	-2.489	4.798	24.004	1.00	34.28	B
ATOM	2681	CE	LYS	B	46	-1.796	3.634	23.340	1.00	40.99	B
ATOM	2682	NZ	LYS	B	46	-1.673	2.499	24.304	1.00	43.75	B
ATOM	2683	C	LYS	B	46	-3.736	8.513	21.798	1.00	28.64	B
ATOM	2684	O	LYS	B	46	-4.951	8.330	21.781	1.00	29.34	B
ATOM	2685	N	ILE	B	47	-3.012	8.691	20.704	1.00	24.97	B
ATOM	2686	CA	ILE	B	47	-3.598	8.725	19.376	1.00	25.58	B
ATOM	2687	CB	ILE	B	47	-3.143	10.009	18.638	1.00	26.32	B
ATOM	2688	CG2	ILE	B	47	-3.793	10.094	17.273	1.00	29.39	B
ATOM	2689	CG1	ILE	B	47	-3.479	11.238	19.480	1.00	31.58	B
ATOM	2690	CD1	ILE	B	47	-2.871	12.534	18.947	1.00	31.25	B
ATOM	2691	C	ILE	B	47	-3.189	7.516	18.539	1.00	25.23	B
ATOM	2692	O	ILE	B	47	-1.999	7.267	18.353	1.00	25.29	B
ATOM	2693	N	TYR	B	48	-4.174	6.766	18.045	1.00	22.75	B
ATOM	2694	CA	TYR	B	48	-3.906	5.612	17.192	1.00	26.17	B
ATOM	2695	CB	TYR	B	48	-4.874	4.460	17.466	1.00	28.61	B
ATOM	2696	CG	TYR	B	48	-4.603	3.692	18.734	1.00	30.76	B
ATOM	2697	CD1	TYR	B	48	-5.141	4.100	19.951	1.00	31.99	B
ATOM	2698	CE1	TYR	B	48	-4.878	3.392	21.128	1.00	37.66	B
ATOM	2699	CD2	TYR	B	48	-3.794	2.559	18.715	1.00	36.38	B
ATOM	2700	CE2	TYR	B	48	-3.522	1.846	19.876	1.00	37.70	B
ATOM	2701	CZ	TYR	B	48	-4.066	2.268	21.077	1.00	37.74	B
ATOM	2702	OH	TYR	B	48	-3.784	1.565	22.221	1.00	43.38	B
ATOM	2703	C	TYR	B	48	-4.059	6.016	15.732	1.00	27.46	B
ATOM	2704	O	TYR	B	48	-5.067	6.602	15.346	1.00	30.28	B
ATOM	2705	N	VAL	B	49	-3.060	5.702	14.918	1.00	29.09	B
ATOM	2706	CA	VAL	B	49	-3.130	6.030	13.512	1.00	26.95	B
ATOM	2707	CB	VAL	B	49	-1.778	6.539	12.983	1.00	25.94	B
ATOM	2708	CG1	VAL	B	49	-1.840	6.721	11.476	1.00	25.67	B
ATOM	2709	CG2	VAL	B	49	-1.437	7.853	13.648	1.00	28.91	B
ATOM	2710	C	VAL	B	49	-3.543	4.770	12.775	1.00	30.78	B
ATOM	2711	O	VAL	B	49	-2.750	3.834	12.608	1.00	29.62	B
ATOM	2712	N	ASN	B	50	-4.796	4.756	12.333	1.00	30.37	B
ATOM	2713	CA	ASN	B	50	-5.335	3.603	11.635	1.00	35.67	B
ATOM	2714	CB	ASN	B	50	-6.588	3.115	12.358	1.00	38.72	B
ATOM	2715	CG	ASN	B	50	-7.044	1.753	11.877	1.00	47.92	B
ATOM	2716	OD1	ASN	B	50	-6.224	.866	11.621	1.00	48.47	B
ATOM	2717	ND2	ASN	B	50	-8.362	1.571	11.767	1.00	51.68	B
ATOM	2718	C	ASN	B	50	-5.648	3.903	10.177	1.00	37.07	B
ATOM	2719	O	ASN	B	50	-6.728	3.596	9.690	1.00	39.72	B
ATOM	2720	N	GLY	B	51	-4.693	4.502	9.482	1.00	39.24	B
ATOM	2721	CA	GLY	B	51	-4.887	4.824	8.083	1.00	39.25	B
ATOM	2722	C	GLY	B	51	-3.613	5.390	7.490	1.00	38.59	B
ATOM	2723	O	GLY	B	51	-2.596	5.486	8.176	1.00	39.44	B
ATOM	2724	N	THR	B	52	-3.650	5.759	6.215	1.00	35.76	B
ATOM	2725	CA	THR	B	52	-2.467	6.311	5.577	1.00	32.36	B
ATOM	2726	CB	THR	B	52	-2.293	5.769	4.152	1.00	32.02	B
ATOM	2727	OG1	THR	B	52	-2.167	4.346	4.201	1.00	31.76	B
ATOM	2728	CG2	THR	B	52	-1.041	6.346	3.514	1.00	27.55	B
ATOM	2729	C	THR	B	52	-2.545	7.827	5.539	1.00	31.72	B
ATOM	2730	O	THR	B	52	-3.438	8.400	4.919	1.00	31.50	B
ATOM	2731	N	ILE	B	53	-1.614	8.466	6.238	1.00	31.14	B
ATOM	2732	CA	ILE	B	53	-1.549	9.917	6.302	1.00	29.55	B
ATOM	2733	CB	ILE	B	53	-.807	10.406	7.561	1.00	29.83	B
ATOM	2734	CG2	ILE	B	53	-.867	11.919	7.638	1.00	25.62	B
ATOM	2735	CG1	ILE	B	53	-1.384	9.737	8.816	1.00	34.95	B
ATOM	2736	CD1	ILE	B	53	-2.839	10.008	9.074	1.00	31.02	B
ATOM	2737	C	ILE	B	53	-.737	10.368	5.099	1.00	33.41	B
ATOM	2738	O	ILE	B	53	.363	9.866	4.864	1.00	30.52	B
ATOM	2739	N	THR	B	54	-1.279	11.320	4.347	1.00	32.64	B
ATOM	2740	CA	THR	B	54	-.589	11.832	3.174	1.00	34.44	B
ATOM	2741	CB	THR	B	54	-1.097	11.155	1.882	1.00	32.67	B
ATOM	2742	OG1	THR	B	54	-2.476	11.474	1.680	1.00	31.84	B
ATOM	2743	CG2	THR	B	54	-.946	9.649	1.977	1.00	34.25	B
ATOM	2744	C	THR	B	54	-.778	13.332	3.028	1.00	32.36	B
ATOM	2745	O	THR	B	54	-1.463	13.973	3.825	1.00	27.60	B
ATOM	2746	N	THR	B	55	-.151	13.887	2.000	1.00	34.77	B
ATOM	2747	CA	THR	B	55	-.263	15.309	1.728	1.00	38.59	B
ATOM	2748	CB	THR	B	55	.766	15.749	.664	1.00	43.08	B

ATOM	2749	OG1	THR	B	55	.715	14.850	-.453	1.00	37.29	B
ATOM	2750	CG2	THR	B	55	2.170	15.755	1.249	1.00	42.12	B
ATOM	2751	C	THR	B	55	-1.679	15.590	1.225	1.00	36.27	B
ATOM	2752	O	THR	B	55	-2.155	16.720	1.287	1.00	36.42	B
ATOM	2753	N	SER	B	56	-2.348	14.544	.745	1.00	35.49	B
ATOM	2754	CA	SER	B	56	-3.715	14.660	.247	1.00	38.32	B
ATOM	2755	CB	SER	B	56	-4.098	13.432	-.577	1.00	40.83	B
ATOM	2756	OG	SER	B	56	-3.410	13.421	-1.813	1.00	51.63	B
ATOM	2757	C	SER	B	56	-4.741	14.830	1.351	1.00	39.06	B
ATOM	2758	O	SER	B	56	-5.770	15.476	1.134	1.00	36.34	B
ATOM	2759	N	ASN	B	57	-4.492	14.234	2.521	1.00	34.86	B
ATOM	2760	CA	ASN	B	57	-5.432	14.369	3.635	1.00	30.12	B
ATOM	2761	CB	ASN	B	57	-5.930	12.999	4.108	1.00	29.57	B
ATOM	2762	CG	ASN	B	57	-4.804	12.077	4.535	1.00	27.24	B
ATOM	2763	OD1	ASN	B	57	-3.845	12.501	5.178	1.00	30.57	B
ATOM	2764	ND2	ASN	B	57	-4.926	10.803	4.190	1.00	28.29	B
ATOM	2765	C	ASN	B	57	-4.852	15.150	4.812	1.00	33.73	B
ATOM	2766	O	ASN	B	57	-5.303	15.008	5.946	1.00	35.34	B
ATOM	2767	N	THR	B	58	-3.854	15.983	4.532	1.00	32.49	B
ATOM	2768	CA	THR	B	58	-3.224	16.814	5.553	1.00	35.41	B
ATOM	2769	CB	THR	B	58	-1.797	16.326	5.889	1.00	30.92	B
ATOM	2770	OG1	THR	B	58	-1.839	14.959	6.300	1.00	31.07	B
ATOM	2771	CG2	THR	B	58	-1.205	17.164	7.010	1.00	30.76	B
ATOM	2772	C	THR	B	58	-3.135	18.248	5.028	1.00	38.11	B
ATOM	2773	O	THR	B	58	-2.535	18.492	3.982	1.00	36.44	B
ATOM	2774	N	SER	B	59	-3.714	19.190	5.765	1.00	36.26	B
ATOM	2775	CA	SER	B	59	-3.722	20.590	5.369	1.00	39.08	B
ATOM	2776	CB	SER	B	59	-4.926	21.307	5.977	1.00	38.39	B
ATOM	2777	OG	SER	B	59	-6.138	20.758	5.493	1.00	43.61	B
ATOM	2778	C	SER	B	59	-2.458	21.332	5.761	1.00	41.93	B
ATOM	2779	O	SER	B	59	-2.386	22.554	5.635	1.00	48.39	B
ATOM	2780	N	ALA	B	60	-1.462	20.609	6.250	1.00	41.64	B
ATOM	2781	CA	ALA	B	60	-.208	21.236	6.635	1.00	36.50	B
ATOM	2782	CB	ALA	B	60	-.022	21.152	8.143	1.00	39.88	B
ATOM	2783	C	ALA	B	60	.928	20.526	5.917	1.00	35.74	B
ATOM	2784	O	ALA	B	60	.736	19.448	5.364	1.00	33.10	B
ATOM	2785	N	SER	B	61	2.113	21.123	5.915	1.00	32.73	B
ATOM	2786	CA	SER	B	61	3.254	20.503	5.248	1.00	38.17	B
ATOM	2787	CB	SER	B	61	4.288	21.566	4.879	1.00	36.31	B
ATOM	2788	OG	SER	B	61	4.816	22.172	6.046	1.00	42.26	B
ATOM	2789	C	SER	B	61	3.903	19.427	6.121	1.00	37.24	B
ATOM	2790	O	SER	B	61	4.780	18.691	5.663	1.00	36.06	B
ATOM	2791	N	LYS	B	62	3.469	19.345	7.379	1.00	37.95	B
ATOM	2792	CA	LYS	B	62	3.987	18.355	8.327	1.00	37.61	B
ATOM	2793	CB	LYS	B	62	5.422	18.698	8.720	1.00	36.51	B
ATOM	2794	CG	LYS	B	62	5.584	20.078	9.324	1.00	42.79	B
ATOM	2795	CD	LYS	B	62	7.046	20.378	9.618	1.00	45.85	B
ATOM	2796	CE	LYS	B	62	7.275	21.890	9.767	1.00	47.50	B
ATOM	2797	NZ	LYS	B	62	6.364	22.498	10.783	1.00	49.41	B
ATOM	2798	C	LYS	B	62	3.121	18.284	9.586	1.00	37.81	B
ATOM	2799	O	LYS	B	62	2.302	19.173	9.841	1.00	33.48	B
ATOM	2800	N	ILE	B	63	3.296	17.219	10.367	1.00	34.70	B
ATOM	2801	CA	ILE	B	63	2.532	17.050	11.595	1.00	29.73	B
ATOM	2802	CB	ILE	B	63	2.268	15.563	11.902	1.00	35.19	B
ATOM	2803	CG2	ILE	B	63	1.433	15.437	13.167	1.00	31.04	B
ATOM	2804	CG1	ILE	B	63	1.561	14.895	10.716	1.00	31.00	B
ATOM	2805	CD1	ILE	B	63	.214	15.484	10.384	1.00	33.56	B
ATOM	2806	C	ILE	B	63	3.343	17.640	12.737	1.00	31.93	B
ATOM	2807	O	ILE	B	63	4.366	17.077	13.139	1.00	26.26	B
ATOM	2808	N	ASP	B	64	2.882	18.775	13.253	1.00	28.35	B
ATOM	2809	CA	ASP	B	64	3.564	19.456	14.341	1.00	28.00	B
ATOM	2810	CB	ASP	B	64	3.338	20.975	14.273	1.00	30.00	B
ATOM	2811	CG	ASP	B	64	4.125	21.648	13.173	1.00	32.18	B
ATOM	2812	OD1	ASP	B	64	5.365	21.632	13.222	1.00	36.27	B
ATOM	2813	OD2	ASP	B	64	3.496	22.207	12.252	1.00	42.51	B
ATOM	2814	C	ASP	B	64	3.114	18.997	15.716	1.00	27.78	B
ATOM	2815	O	ASP	B	64	1.947	19.132	16.074	1.00	24.49	B
ATOM	2816	N	VAL	B	65	4.049	18.460	16.487	1.00	26.96	B
ATOM	2817	CA	VAL	B	65	3.761	18.061	17.859	1.00	28.08	B

ATOM	2818	CB	VAL	B	65	4.394	16.701	18.199	1.00	25.84	B
ATOM	2819	CG1	VAL	B	65	4.053	16.311	19.621	1.00	25.48	B
ATOM	2820	CG2	VAL	B	65	3.887	15.648	17.238	1.00	26.92	B
ATOM	2821	C	VAL	B	65	4.444	19.165	18.657	1.00	29.74	B
ATOM	2822	O	VAL	B	65	5.640	19.083	18.940	1.00	29.13	B
ATOM	2823	N	LYS	B	66	3.696	20.216	18.989	1.00	26.52	B
ATOM	2824	CA	LYS	B	66	4.286	21.329	19.716	1.00	30.33	B
ATOM	2825	CB	LYS	B	66	4.750	22.413	18.733	1.00	36.59	B
ATOM	2826	CG	LYS	B	66	3.688	23.411	18.302	1.00	45.19	B
ATOM	2827	CD	LYS	B	66	4.349	24.577	17.576	1.00	48.36	B
ATOM	2828	CE	LYS	B	66	3.361	25.694	17.261	1.00	53.27	B
ATOM	2829	NZ	LYS	B	66	4.040	26.887	16.634	1.00	54.43	B
ATOM	2830	C	LYS	B	66	3.388	21.941	20.783	1.00	28.41	B
ATOM	2831	O	LYS	B	66	2.163	21.995	20.644	1.00	28.16	B
ATOM	2832	N	ASP	B	67	4.018	22.405	21.853	1.00	26.28	B
ATOM	2833	CA	ASP	B	67	3.298	22.991	22.975	1.00	34.01	B
ATOM	2834	CB	ASP	B	67	2.572	24.270	22.549	1.00	34.59	B
ATOM	2835	CG	ASP	B	67	3.526	25.337	22.067	1.00	36.51	B
ATOM	2836	OD1	ASP	B	67	4.499	25.647	22.793	1.00	37.83	B
ATOM	2837	OD2	ASP	B	67	3.301	25.864	20.962	1.00	41.18	B
ATOM	2838	C	ASP	B	67	2.307	21.997	23.569	1.00	31.99	B
ATOM	2839	O	ASP	B	67	1.187	22.354	23.916	1.00	33.61	B
ATOM	2840	N	VAL	B	68	2.730	20.742	23.669	1.00	30.53	B
ATOM	2841	CA	VAL	B	68	1.901	19.695	24.249	1.00	30.65	B
ATOM	2842	CB	VAL	B	68	1.190	18.845	23.175	1.00	31.07	B
ATOM	2843	CG1	VAL	B	68	.139	19.673	22.474	1.00	35.51	B
ATOM	2844	CG2	VAL	B	68	2.204	18.310	22.183	1.00	28.96	B
ATOM	2845	C	VAL	B	68	2.785	18.789	25.092	1.00	30.41	B
ATOM	2846	O	VAL	B	68	4.008	18.773	24.935	1.00	28.25	B
ATOM	2847	N	SER	B	69	2.159	18.047	25.992	1.00	27.85	B
ATOM	2848	CA	SER	B	69	2.889	17.141	26.868	1.00	28.65	B
ATOM	2849	CB	SER	B	69	3.196	17.816	28.205	1.00	27.67	B
ATOM	2850	OG	SER	B	69	4.207	18.791	28.061	1.00	34.25	B
ATOM	2851	C	SER	B	69	2.098	15.879	27.134	1.00	26.31	B
ATOM	2852	O	SER	B	69	.861	15.886	27.073	1.00	25.92	B
ATOM	2853	N	ASN	B	70	2.818	14.800	27.425	1.00	21.66	B
ATOM	2854	CA	ASN	B	70	2.197	13.522	27.738	1.00	24.83	B
ATOM	2855	CB	ASN	B	70	1.381	13.690	29.019	1.00	22.45	B
ATOM	2856	CG	ASN	B	70	2.109	14.542	30.046	1.00	26.64	B
ATOM	2857	OD1	ASN	B	70	3.230	14.227	30.432	1.00	26.28	B
ATOM	2858	ND2	ASN	B	70	1.484	15.631	30.477	1.00	23.01	B
ATOM	2859	C	ASN	B	70	1.322	13.057	26.576	1.00	26.39	B
ATOM	2860	O	ASN	B	70	.094	13.009	26.674	1.00	25.63	B
ATOM	2861	N	VAL	B	71	1.979	12.697	25.480	1.00	26.34	B
ATOM	2862	CA	VAL	B	71	1.294	12.259	24.279	1.00	22.21	B
ATOM	2863	CB	VAL	B	71	1.293	13.379	23.209	1.00	25.99	B
ATOM	2864	CG1	VAL	B	71	.777	12.844	21.887	1.00	21.99	B
ATOM	2865	CG2	VAL	B	71	.438	14.560	23.678	1.00	24.25	B
ATOM	2866	C	VAL	B	71	1.925	11.030	23.648	1.00	25.28	B
ATOM	2867	O	VAL	B	71	3.142	10.872	23.637	1.00	23.21	B
ATOM	2868	N	SER	B	72	1.082	10.162	23.115	1.00	22.20	B
ATOM	2869	CA	SER	B	72	1.555	8.982	22.425	1.00	22.18	B
ATOM	2870	CB	SER	B	72	1.186	7.703	23.181	1.00	18.46	B
ATOM	2871	OG	SER	B	72	1.975	7.536	24.336	1.00	24.95	B
ATOM	2872	C	SER	B	72	.901	8.952	21.050	1.00	26.05	B
ATOM	2873	O	SER	B	72	-.325	9.081	20.935	1.00	24.45	B
ATOM	2874	N	ILE	B	73	1.715	8.818	20.009	1.00	20.54	B
ATOM	2875	CA	ILE	B	73	1.200	8.721	18.651	1.00	19.28	B
ATOM	2876	CB	ILE	B	73	1.777	9.811	17.733	1.00	25.60	B
ATOM	2877	CG2	ILE	B	73	1.294	9.590	16.303	1.00	25.44	B
ATOM	2878	CG1	ILE	B	73	1.352	11.194	18.240	1.00	24.61	B
ATOM	2879	CD1	ILE	B	73	1.872	12.331	17.400	1.00	30.73	B
ATOM	2880	C	ILE	B	73	1.672	7.359	18.197	1.00	19.05	B
ATOM	2881	O	ILE	B	73	2.857	7.160	17.940	1.00	22.75	B
ATOM	2882	N	VAL	B	74	.742	6.416	18.118	1.00	19.87	B
ATOM	2883	CA	VAL	B	74	1.074	5.045	17.759	1.00	21.70	B
ATOM	2884	CB	VAL	B	74	.925	4.113	18.993	1.00	25.72	B
ATOM	2885	CG1	VAL	B	74	1.800	4.601	20.134	1.00	29.52	B
ATOM	2886	CG2	VAL	B	74	-.513	4.082	19.442	1.00	28.80	B

ATOM	2887	C	VAL	B	74	.227	4.471	16.633	1.00	22.30	B
ATOM	2888	O	VAL	B	74	-.964	4.751	16.526	1.00	24.05	B
ATOM	2889	N	GLY	B	75	.850	3.653	15.798	1.00	24.28	B
ATOM	2890	CA	GLY	B	75	.123	3.036	14.710	1.00	24.00	B
ATOM	2891	C	GLY	B	75	-.591	1.786	15.203	1.00	31.63	B
ATOM	2892	O	GLY	B	75	-.125	1.119	16.134	1.00	27.46	B
ATOM	2893	N	SER	B	76	-1.738	1.474	14.609	1.00	29.90	B
ATOM	2894	CA	SER	B	76	-2.462	.275	15.004	1.00	34.65	B
ATOM	2895	CB	SER	B	76	-3.971	.526	15.029	1.00	33.53	B
ATOM	2896	OG	SER	B	76	-4.402	1.085	13.808	1.00	44.04	B
ATOM	2897	C	SER	B	76	-2.126	-.812	14.001	1.00	36.08	B
ATOM	2898	O	SER	B	76	-2.170	-.587	12.785	1.00	32.95	B
ATOM	2899	N	GLY	B	77	-1.773	-1.986	14.516	1.00	34.01	B
ATOM	2900	CA	GLY	B	77	-1.421	-3.083	13.640	1.00	36.17	B
ATOM	2901	C	GLY	B	77	-.283	-2.657	12.741	1.00	39.04	B
ATOM	2902	O	GLY	B	77	.749	-2.162	13.216	1.00	39.37	B
ATOM	2903	N	THR	B	78	-.467	-2.845	11.438	1.00	37.75	B
ATOM	2904	CA	THR	B	78	.548	-2.466	10.469	1.00	37.71	B
ATOM	2905	CB	THR	B	78	1.031	-3.683	9.625	1.00	39.59	B
ATOM	2906	OG1	THR	B	78	-.067	-4.216	8.871	1.00	41.18	B
ATOM	2907	CG2	THR	B	78	1.581	-4.771	10.522	1.00	38.93	B
ATOM	2908	C	THR	B	78	-.045	-1.427	9.530	1.00	37.54	B
ATOM	2909	O	THR	B	78	.429	-1.260	8.406	1.00	40.60	B
ATOM	2910	N	LYS	B	79	-1.083	-.735	10.002	1.00	35.80	B
ATOM	2911	CA	LYS	B	79	-1.759	.294	9.214	1.00	34.15	B
ATOM	2912	CB	LYS	B	79	-3.277	.141	9.347	1.00	38.33	B
ATOM	2913	CG	LYS	B	79	-3.821	-1.245	8.984	1.00	48.72	B
ATOM	2914	CD	LYS	B	79	-3.164	-1.808	7.710	1.00	55.76	B
ATOM	2915	CE	LYS	B	79	-3.879	-3.084	7.234	1.00	60.09	B
ATOM	2916	NZ	LYS	B	79	-4.214	-3.991	8.376	1.00	62.45	B
ATOM	2917	C	LYS	B	79	-1.372	1.737	9.569	1.00	32.28	B
ATOM	2918	O	LYS	B	79	-1.903	2.686	8.983	1.00	29.62	B
ATOM	2919	N	GLY	B	80	-.461	1.908	10.523	1.00	29.61	B
ATOM	2920	CA	GLY	B	80	-.034	3.245	10.902	1.00	27.19	B
ATOM	2921	C	GLY	B	80	1.021	3.725	9.928	1.00	28.63	B
ATOM	2922	O	GLY	B	80	2.202	3.414	10.082	1.00	30.98	B
ATOM	2923	N	GLU	B	81	.609	4.487	8.920	1.00	27.06	B
ATOM	2924	CA	GLU	B	81	1.562	4.965	7.925	1.00	28.12	B
ATOM	2925	CB	GLU	B	81	1.448	4.116	6.663	1.00	26.31	B
ATOM	2926	CG	GLU	B	81	2.283	4.617	5.496	1.00	30.75	B
ATOM	2927	CD	GLU	B	81	2.081	3.781	4.245	1.00	40.03	B
ATOM	2928	OE1	GLU	B	81	.983	3.208	4.100	1.00	39.05	B
ATOM	2929	OE2	GLU	B	81	3.002	3.707	3.401	1.00	43.65	B
ATOM	2930	C	GLU	B	81	1.495	6.442	7.532	1.00	28.19	B
ATOM	2931	O	GLU	B	81	.417	7.002	7.310	1.00	27.89	B
ATOM	2932	N	LEU	B	82	2.673	7.058	7.452	1.00	27.43	B
ATOM	2933	CA	LEU	B	82	2.801	8.451	7.040	1.00	31.18	B
ATOM	2934	CB	LEU	B	82	3.526	9.291	8.095	1.00	24.55	B
ATOM	2935	CG	LEU	B	82	2.663	9.806	9.251	1.00	27.41	B
ATOM	2936	CD1	LEU	B	82	2.193	8.638	10.092	1.00	26.23	B
ATOM	2937	CD2	LEU	B	82	3.461	10.787	10.093	1.00	24.98	B
ATOM	2938	C	LEU	B	82	3.610	8.422	5.756	1.00	31.72	B
ATOM	2939	O	LEU	B	82	4.813	8.158	5.775	1.00	29.76	B
ATOM	2940	N	LYS	B	83	2.936	8.683	4.644	1.00	30.86	B
ATOM	2941	CA	LYS	B	83	3.572	8.665	3.332	1.00	33.20	B
ATOM	2942	CB	LYS	B	83	2.742	7.786	2.395	1.00	35.57	B
ATOM	2943	CG	LYS	B	83	3.246	7.706	.962	1.00	43.66	B
ATOM	2944	CD	LYS	B	83	2.429	6.691	.170	1.00	48.96	B
ATOM	2945	CE	LYS	B	83	2.861	6.626	-1.296	1.00	54.64	B
ATOM	2946	NZ	LYS	B	83	2.202	5.492	-2.024	1.00	57.32	B
ATOM	2947	C	LYS	B	83	3.725	10.072	2.754	1.00	29.97	B
ATOM	2948	O	LYS	B	83	2.737	10.744	2.463	1.00	27.79	B
ATOM	2949	N	GLY	B	84	4.974	10.507	2.603	1.00	28.73	B
ATOM	2950	CA	GLY	B	84	5.249	11.822	2.059	1.00	29.79	B
ATOM	2951	C	GLY	B	84	5.085	12.944	3.067	1.00	33.12	B
ATOM	2952	O	GLY	B	84	5.324	14.112	2.747	1.00	34.95	B
ATOM	2953	N	ILE	B	85	4.682	12.600	4.288	1.00	33.66	B
ATOM	2954	CA	ILE	B	85	4.490	13.591	5.341	1.00	33.56	B
ATOM	2955	CB	ILE	B	85	2.979	13.736	5.692	1.00	36.94	B

ATOM	2956	CG2	ILE	B	85	2.597	12.852	6.889	1.00	45.01	B
ATOM	2957	CG1	ILE	B	85	2.658	15.193	6.005	1.00	41.89	B
ATOM	2958	CD1	ILE	B	85	2.425	16.015	4.765	1.00	40.82	B
ATOM	2959	C	ILE	B	85	5.293	13.179	6.587	1.00	34.94	B
ATOM	2960	O	ILE	B	85	5.312	12.003	6.975	1.00	34.23	B
ATOM	2961	N	GLY	B	86	5.952	14.148	7.213	1.00	29.10	B
ATOM	2962	CA	GLY	B	86	6.753	13.844	8.384	1.00	28.36	B
ATOM	2963	C	GLY	B	86	6.236	14.413	9.692	1.00	30.26	B
ATOM	2964	O	GLY	B	86	5.216	15.098	9.730	1.00	30.69	B
ATOM	2965	N	ILE	B	87	6.956	14.127	10.768	1.00	25.91	B
ATOM	2966	CA	ILE	B	87	6.600	14.602	12.098	1.00	25.13	B
ATOM	2967	CB	ILE	B	87	6.384	13.411	13.069	1.00	25.26	B
ATOM	2968	CG2	ILE	B	87	6.196	13.916	14.495	1.00	26.57	B
ATOM	2969	CG1	ILE	B	87	5.172	12.594	12.632	1.00	28.59	B
ATOM	2970	CD1	ILE	B	87	4.948	11.338	13.456	1.00	33.41	B
ATOM	2971	C	ILE	B	87	7.700	15.495	12.676	1.00	25.27	B
ATOM	2972	O	ILE	B	87	8.890	15.190	12.573	1.00	26.31	B
ATOM	2973	N	LYS	B	88	7.297	16.597	13.291	1.00	24.70	B
ATOM	2974	CA	LYS	B	88	8.250	17.504	13.908	1.00	25.87	B
ATOM	2975	CB	LYS	B	88	8.294	18.838	13.160	1.00	29.93	B
ATOM	2976	CG	LYS	B	88	9.248	19.844	13.782	1.00	34.93	B
ATOM	2977	CD	LYS	B	88	9.091	21.222	13.167	1.00	42.12	B
ATOM	2978	CE	LYS	B	88	9.983	22.248	13.851	1.00	42.20	B
ATOM	2979	NZ	LYS	B	88	11.414	21.849	13.771	1.00	47.27	B
ATOM	2980	C	LYS	B	88	7.824	17.739	15.357	1.00	28.00	B
ATOM	2981	O	LYS	B	88	6.721	18.233	15.618	1.00	26.78	B
ATOM	2982	N	ILE	B	89	8.695	17.361	16.289	1.00	24.62	B
ATOM	2983	CA	ILE	B	89	8.446	17.533	17.721	1.00	25.38	B
ATOM	2984	CB	ILE	B	89	8.897	16.287	18.505	1.00	24.39	B
ATOM	2985	CG2	ILE	B	89	8.668	16.490	19.991	1.00	25.66	B
ATOM	2986	CG1	ILE	B	89	8.118	15.069	18.011	1.00	26.14	B
ATOM	2987	CD1	ILE	B	89	8.615	13.761	18.564	1.00	27.51	B
ATOM	2988	C	ILE	B	89	9.230	18.752	18.196	1.00	26.58	B
ATOM	2989	O	ILE	B	89	10.448	18.815	18.039	1.00	28.11	B
ATOM	2990	N	TRP	B	90	8.530	19.709	18.793	1.00	26.79	B
ATOM	2991	CA	TRP	B	90	9.151	20.954	19.232	1.00	28.37	B
ATOM	2992	CB	TRP	B	90	9.151	21.896	18.018	1.00	34.71	B
ATOM	2993	CG	TRP	B	90	9.659	23.277	18.216	1.00	47.15	B
ATOM	2994	CD2	TRP	B	90	9.111	24.473	17.642	1.00	50.58	B
ATOM	2995	CE2	TRP	B	90	9.929	25.549	18.054	1.00	53.78	B
ATOM	2996	CE3	TRP	B	90	8.008	24.735	16.816	1.00	55.56	B
ATOM	2997	CD1	TRP	B	90	10.760	23.665	18.931	1.00	49.54	B
ATOM	2998	NE1	TRP	B	90	10.927	25.030	18.838	1.00	51.05	B
ATOM	2999	CZ2	TRP	B	90	9.679	26.877	17.670	1.00	57.72	B
ATOM	3000	CZ3	TRP	B	90	7.755	26.056	16.428	1.00	58.41	B
ATOM	3001	CH2	TRP	B	90	8.590	27.111	16.859	1.00	59.86	B
ATOM	3002	C	TRP	B	90	8.403	21.549	20.439	1.00	26.49	B
ATOM	3003	O	TRP	B	90	7.181	21.630	20.448	1.00	26.38	B
ATOM	3004	N	ARG	B	91	9.151	21.960	21.455	1.00	25.51	B
ATOM	3005	CA	ARG	B	91	8.576	22.515	22.676	1.00	29.08	B
ATOM	3006	CB	ARG	B	91	7.936	23.878	22.413	1.00	29.52	B
ATOM	3007	CG	ARG	B	91	8.890	24.905	21.829	1.00	39.35	B
ATOM	3008	CD	ARG	B	91	8.457	26.319	22.187	1.00	40.13	B
ATOM	3009	NE	ARG	B	91	7.071	26.581	21.815	1.00	42.61	B
ATOM	3010	CZ	ARG	B	91	6.650	26.772	20.567	1.00	49.58	B
ATOM	3011	NH1	ARG	B	91	7.507	26.732	19.558	1.00	51.49	B
ATOM	3012	NH2	ARG	B	91	5.367	27.010	20.326	1.00	51.74	B
ATOM	3013	C	ARG	B	91	7.533	21.552	23.227	1.00	29.72	B
ATOM	3014	O	ARG	B	91	6.412	21.943	23.550	1.00	26.80	B
ATOM	3015	N	ALA	B	92	7.921	20.285	23.324	1.00	27.79	B
ATOM	3016	CA	ALA	B	92	7.042	19.229	23.815	1.00	28.29	B
ATOM	3017	CB	ALA	B	92	6.507	18.424	22.649	1.00	21.22	B
ATOM	3018	C	ALA	B	92	7.809	18.312	24.769	1.00	28.00	B
ATOM	3019	O	ALA	B	92	9.011	18.106	24.609	1.00	30.10	B
ATOM	3020	N	ASN	B	93	7.121	17.764	25.761	1.00	23.77	B
ATOM	3021	CA	ASN	B	93	7.773	16.878	26.719	1.00	26.01	B
ATOM	3022	CB	ASN	B	93	7.929	17.576	28.072	1.00	34.26	B
ATOM	3023	CG	ASN	B	93	8.718	18.861	27.971	1.00	44.02	B
ATOM	3024	OD1	ASN	B	93	9.837	18.874	27.449	1.00	52.92	B

ATOM	3025	ND2	ASN	B	93	8.142	19.954	28.463	1.00	49.69	B
ATOM	3026	C	ASN	B	93	6.989	15.594	26.916	1.00	25.13	B
ATOM	3027	O	ASN	B	93	5.767	15.586	26.791	1.00	22.46	B
ATOM	3028	N	ASN	B	94	7.702	14.517	27.239	1.00	22.68	B
ATOM	3029	CA	ASN	B	94	7.085	13.215	27.479	1.00	22.90	B
ATOM	3030	CB	ASN	B	94	6.244	13.260	28.763	1.00	19.65	B
ATOM	3031	CG	ASN	B	94	5.721	11.893	29.160	1.00	24.72	B
ATOM	3032	OD1	ASN	B	94	6.347	10.878	28.869	1.00	21.72	B
ATOM	3033	ND2	ASN	B	94	4.578	11.860	29.833	1.00	18.28	B
ATOM	3034	C	ASN	B	94	6.222	12.787	26.294	1.00	24.00	B
ATOM	3035	O	ASN	B	94	4.994	12.717	26.387	1.00	21.38	B
ATOM	3036	N	ILE	B	95	6.895	12.494	25.187	1.00	22.47	B
ATOM	3037	CA	ILE	B	95	6.245	12.104	23.949	1.00	20.41	B
ATOM	3038	CB	ILE	B	95	6.560	13.129	22.818	1.00	23.75	B
ATOM	3039	CG2	ILE	B	95	5.802	12.765	21.556	1.00	22.30	B
ATOM	3040	CG1	ILE	B	95	6.193	14.549	23.264	1.00	19.90	B
ATOM	3041	CD1	ILE	B	95	4.745	14.743	23.586	1.00	19.71	B
ATOM	3042	C	ILE	B	95	6.715	10.720	23.493	1.00	22.50	B
ATOM	3043	O	ILE	B	95	7.896	10.381	23.594	1.00	20.80	B
ATOM	3044	N	ILE	B	96	5.779	9.925	22.993	1.00	18.66	B
ATOM	3045	CA	ILE	B	96	6.088	8.599	22.499	1.00	20.23	B
ATOM	3046	CB	ILE	B	96	5.424	7.514	23.363	1.00	21.47	B
ATOM	3047	CG2	ILE	B	96	5.572	6.150	22.694	1.00	18.02	B
ATOM	3048	CG1	ILE	B	96	6.056	7.494	24.761	1.00	22.39	B
ATOM	3049	CD1	ILE	B	96	5.519	6.393	25.649	1.00	18.24	B
ATOM	3050	C	ILE	B	96	5.610	8.435	21.050	1.00	20.32	B
ATOM	3051	O	ILE	B	96	4.450	8.703	20.739	1.00	22.01	B
ATOM	3052	N	ILE	B	97	6.522	8.016	20.177	1.00	18.30	B
ATOM	3053	CA	ILE	B	97	6.219	7.774	18.766	1.00	19.28	B
ATOM	3054	CB	ILE	B	97	7.126	8.596	17.823	1.00	18.70	B
ATOM	3055	CG2	ILE	B	97	6.690	8.383	16.381	1.00	19.06	B
ATOM	3056	CG1	ILE	B	97	7.060	10.085	18.180	1.00	20.72	B
ATOM	3057	CD1	ILE	B	97	5.706	10.708	17.987	1.00	16.35	B
ATOM	3058	C	ILE	B	97	6.507	6.298	18.549	1.00	20.79	B
ATOM	3059	O	ILE	B	97	7.660	5.867	18.601	1.00	21.89	B
ATOM	3060	N	ARG	B	98	5.462	5.526	18.279	1.00	21.12	B
ATOM	3061	CA	ARG	B	98	5.634	4.089	18.134	1.00	22.33	B
ATOM	3062	CB	ARG	B	98	5.369	3.421	19.491	1.00	19.43	B
ATOM	3063	CG	ARG	B	98	5.239	1.898	19.448	1.00	26.43	B
ATOM	3064	CD	ARG	B	98	5.761	1.267	20.741	1.00	30.85	B
ATOM	3065	NE	ARG	B	98	5.052	1.767	21.909	1.00	33.80	B
ATOM	3066	CZ	ARG	B	98	5.622	2.068	23.074	1.00	33.88	B
ATOM	3067	NH1	ARG	B	98	4.871	2.516	24.061	1.00	32.21	B
ATOM	3068	NH2	ARG	B	98	6.931	1.934	23.253	1.00	28.42	B
ATOM	3069	C	ARG	B	98	4.829	3.368	17.077	1.00	23.52	B
ATOM	3070	O	ARG	B	98	3.698	3.727	16.772	1.00	22.54	B
ATOM	3071	N	ASN	B	99	5.443	2.330	16.526	1.00	21.35	B
ATOM	3072	CA	ASN	B	99	4.793	1.491	15.541	1.00	20.35	B
ATOM	3073	CB	ASN	B	99	3.677	.707	16.233	1.00	20.96	B
ATOM	3074	CG	ASN	B	99	3.263	-.513	15.460	1.00	21.55	B
ATOM	3075	OD1	ASN	B	99	4.106	-1.274	14.988	1.00	21.34	B
ATOM	3076	ND2	ASN	B	99	1.962	-.717	15.333	1.00	22.34	B
ATOM	3077	C	ASN	B	99	4.245	2.235	14.327	1.00	22.29	B
ATOM	3078	O	ASN	B	99	3.111	2.018	13.913	1.00	23.63	B
ATOM	3079	N	LEU	B	100	5.060	3.114	13.756	1.00	26.28	B
ATOM	3080	CA	LEU	B	100	4.652	3.866	12.578	1.00	23.88	B
ATOM	3081	CB	LEU	B	100	4.568	5.358	12.890	1.00	25.97	B
ATOM	3082	CG	LEU	B	100	3.466	5.865	13.814	1.00	24.16	B
ATOM	3083	CD1	LEU	B	100	3.689	7.352	14.078	1.00	24.67	B
ATOM	3084	CD2	LEU	B	100	2.105	5.623	13.179	1.00	23.65	B
ATOM	3085	C	LEU	B	100	5.622	3.673	11.428	1.00	24.85	B
ATOM	3086	O	LEU	B	100	6.811	3.453	11.631	1.00	23.85	B
ATOM	3087	N	LYS	B	101	5.101	3.750	10.213	1.00	25.42	B
ATOM	3088	CA	LYS	B	101	5.934	3.641	9.032	1.00	27.44	B
ATOM	3089	CB	LYS	B	101	5.376	2.596	8.062	1.00	29.44	B
ATOM	3090	CG	LYS	B	101	6.206	2.453	6.798	1.00	35.65	B
ATOM	3091	CD	LYS	B	101	5.575	1.488	5.796	1.00	39.27	B
ATOM	3092	CE	LYS	B	101	5.572	.051	6.302	1.00	44.47	B
ATOM	3093	NZ	LYS	B	101	5.198	-.897	5.202	1.00	45.75	B

ATOM	3094	C	LYS	B	101	5.899	5.024	8.397	1.00	27.23	B
ATOM	3095	O	LYS	B	101	4.872	5.438	7.874	1.00	28.12	B
ATOM	3096	N	ILE	B	102	7.014	5.743	8.473	1.00	26.95	B
ATOM	3097	CA	ILE	B	102	7.108	7.086	7.914	1.00	24.83	B
ATOM	3098	CB	ILE	B	102	7.519	8.091	8.996	1.00	26.40	B
ATOM	3099	CG2	ILE	B	102	7.414	9.515	8.460	1.00	23.74	B
ATOM	3100	CG1	ILE	B	102	6.619	7.912	10.222	1.00	19.70	B
ATOM	3101	CD1	ILE	B	102	7.040	8.726	11.426	1.00	24.77	B
ATOM	3102	C	ILE	B	102	8.158	7.048	6.813	1.00	28.33	B
ATOM	3103	O	ILE	B	102	9.287	6.621	7.049	1.00	22.81	B
ATOM	3104	N	HIS	B	103	7.801	7.509	5.614	1.00	28.99	B
ATOM	3105	CA	HIS	B	103	8.744	7.434	4.503	1.00	28.41	B
ATOM	3106	CB	HIS	B	103	8.696	6.015	3.926	1.00	28.50	B
ATOM	3107	CG	HIS	B	103	7.335	5.608	3.450	1.00	30.79	B
ATOM	3108	CD2	HIS	B	103	6.215	5.276	4.134	1.00	31.57	B
ATOM	3109	ND1	HIS	B	103	7.007	5.517	2.112	1.00	31.72	B
ATOM	3110	CE1	HIS	B	103	5.744	5.143	1.994	1.00	29.33	B
ATOM	3111	NE2	HIS	B	103	5.241	4.990	3.207	1.00	33.13	B
ATOM	3112	C	HIS	B	103	8.597	8.425	3.354	1.00	27.48	B
ATOM	3113	O	HIS	B	103	7.512	8.945	3.095	1.00	26.97	B
ATOM	3114	N	GLU	B	104	9.720	8.657	2.674	1.00	28.36	B
ATOM	3115	CA	GLU	B	104	9.811	9.527	1.499	1.00	30.87	B
ATOM	3116	CB	GLU	B	104	9.265	8.756	.292	1.00	32.12	B
ATOM	3117	CG	GLU	B	104	9.907	7.368	.185	1.00	34.97	B
ATOM	3118	CD	GLU	B	104	9.171	6.413	-.737	1.00	37.81	B
ATOM	3119	OE1	GLU	B	104	9.516	6.353	-1.942	1.00	39.51	B
ATOM	3120	OE2	GLU	B	104	8.245	5.724	-.253	1.00	35.36	B
ATOM	3121	C	GLU	B	104	9.113	10.874	1.665	1.00	28.59	B
ATOM	3122	O	GLU	B	104	8.129	11.168	1.000	1.00	26.86	B
ATOM	3123	N	VAL	B	105	9.657	11.690	2.558	1.00	28.14	B
ATOM	3124	CA	VAL	B	105	9.101	12.999	2.868	1.00	29.00	B
ATOM	3125	CB	VAL	B	105	9.247	13.292	4.390	1.00	27.52	B
ATOM	3126	CG1	VAL	B	105	8.531	14.579	4.754	1.00	24.64	B
ATOM	3127	CG2	VAL	B	105	8.696	12.115	5.202	1.00	27.24	B
ATOM	3128	C	VAL	B	105	9.806	14.093	2.074	1.00	30.14	B
ATOM	3129	O	VAL	B	105	10.902	14.516	2.432	1.00	31.22	B
ATOM	3130	N	ALA	B	106	9.179	14.552	.996	1.00	33.19	B
ATOM	3131	CA	ALA	B	106	9.776	15.598	.168	1.00	38.69	B
ATOM	3132	CB	ALA	B	106	9.561	15.285	-1.300	1.00	39.08	B
ATOM	3133	C	ALA	B	106	9.199	16.969	.491	1.00	38.64	B
ATOM	3134	O	ALA	B	106	9.583	17.967	-.108	1.00	42.80	B
ATOM	3135	N	SER	B	107	8.281	17.015	1.446	1.00	38.47	B
ATOM	3136	CA	SER	B	107	7.643	18.265	1.832	1.00	39.77	B
ATOM	3137	CB	SER	B	107	6.132	18.067	1.848	1.00	41.85	B
ATOM	3138	OG	SER	B	107	5.822	16.847	2.505	1.00	49.22	B
ATOM	3139	C	SER	B	107	8.117	18.752	3.195	1.00	39.26	B
ATOM	3140	O	SER	B	107	8.874	18.067	3.883	1.00	39.26	B
ATOM	3141	N	GLY	B	108	7.671	19.944	3.578	1.00	40.00	B
ATOM	3142	CA	GLY	B	108	8.057	20.498	4.861	1.00	37.30	B
ATOM	3143	C	GLY	B	108	9.557	20.493	5.062	1.00	39.43	B
ATOM	3144	O	GLY	B	108	10.310	20.920	4.181	1.00	37.77	B
ATOM	3145	N	ASP	B	109	9.996	20.009	6.221	1.00	35.76	B
ATOM	3146	CA	ASP	B	109	11.415	19.950	6.547	1.00	33.98	B
ATOM	3147	CB	ASP	B	109	11.594	19.812	8.064	1.00	40.99	B
ATOM	3148	CG	ASP	B	109	11.111	21.040	8.824	1.00	42.81	B
ATOM	3149	OD1	ASP	B	109	11.055	20.998	10.074	1.00	48.38	B
ATOM	3150	OD2	ASP	B	109	10.792	22.055	8.175	1.00	42.01	B
ATOM	3151	C	ASP	B	109	12.118	18.799	5.838	1.00	31.63	B
ATOM	3152	O	ASP	B	109	13.339	18.655	5.935	1.00	30.34	B
ATOM	3153	N	LYS	B	110	11.343	17.982	5.130	1.00	31.00	B
ATOM	3154	CA	LYS	B	110	11.876	16.837	4.390	1.00	34.18	B
ATOM	3155	CB	LYS	B	110	12.876	17.337	3.336	1.00	36.94	B
ATOM	3156	CG	LYS	B	110	12.273	18.374	2.372	1.00	41.41	B
ATOM	3157	CD	LYS	B	110	13.344	19.073	1.534	1.00	46.87	B
ATOM	3158	CE	LYS	B	110	13.749	18.268	.314	1.00	46.54	B
ATOM	3159	NZ	LYS	B	110	12.789	18.447	-.829	1.00	52.51	B
ATOM	3160	C	LYS	B	110	12.527	15.769	5.293	1.00	33.32	B
ATOM	3161	O	LYS	B	110	13.410	15.024	4.861	1.00	31.51	B
ATOM	3162	N	ASP	B	111	12.080	15.703	6.545	1.00	30.50	B

ATOM	3163	CA	ASP	B	111	12.593	14.734	7.513	1.00	27.28	B
ATOM	3164	CB	ASP	B	111	13.110	15.446	8.765	1.00	29.16	B
ATOM	3165	CG	ASP	B	111	14.152	16.502	8.455	1.00	29.28	B
ATOM	3166	OD1	ASP	B	111	14.176	17.541	9.159	1.00	29.64	B
ATOM	3167	OD2	ASP	B	111	14.954	16.291	7.520	1.00	32.03	B
ATOM	3168	C	ASP	B	111	11.454	13.809	7.923	1.00	27.35	B
ATOM	3169	O	ASP	B	111	10.306	14.244	8.024	1.00	27.64	B
ATOM	3170	N	ALA	B	112	11.757	12.535	8.144	1.00	23.18	B
ATOM	3171	CA	ALA	B	112	10.725	11.602	8.578	1.00	24.98	B
ATOM	3172	CB	ALA	B	112	11.284	10.182	8.634	1.00	25.70	B
ATOM	3173	C	ALA	B	112	10.291	12.060	9.970	1.00	25.56	B
ATOM	3174	O	ALA	B	112	9.108	12.288	10.233	1.00	25.31	B
ATOM	3175	N	ILE	B	113	11.272	12.204	10.853	1.00	26.08	B
ATOM	3176	CA	ILE	B	113	11.031	12.663	12.209	1.00	27.92	B
ATOM	3177	CB	ILE	B	113	11.135	11.529	13.250	1.00	25.54	B
ATOM	3178	CG2	ILE	B	113	10.918	12.103	14.649	1.00	27.71	B
ATOM	3179	CG1	ILE	B	113	10.094	10.450	12.974	1.00	28.69	B
ATOM	3180	CD1	ILE	B	113	10.138	9.290	13.960	1.00	25.50	B
ATOM	3181	C	ILE	B	113	12.083	13.696	12.566	1.00	26.53	B
ATOM	3182	O	ILE	B	113	13.282	13.454	12.402	1.00	26.45	B
ATOM	3183	N	GLY	B	114	11.625	14.839	13.059	1.00	26.36	B
ATOM	3184	CA	GLY	B	114	12.534	15.889	13.463	1.00	24.14	B
ATOM	3185	C	GLY	B	114	12.218	16.383	14.865	1.00	26.76	B
ATOM	3186	O	GLY	B	114	11.063	16.639	15.199	1.00	24.25	B
ATOM	3187	N	ILE	B	115	13.246	16.501	15.697	1.00	24.27	B
ATOM	3188	CA	ILE	B	115	13.059	16.989	17.056	1.00	26.57	B
ATOM	3189	CB	ILE	B	115	13.521	15.967	18.113	1.00	26.42	B
ATOM	3190	CG2	ILE	B	115	13.339	16.551	19.504	1.00	24.03	B
ATOM	3191	CG1	ILE	B	115	12.704	14.679	17.993	1.00	26.18	B
ATOM	3192	CD1	ILE	B	115	13.124	13.605	18.974	1.00	27.16	B
ATOM	3193	C	ILE	B	115	13.858	18.268	17.255	1.00	28.36	B
ATOM	3194	O	ILE	B	115	15.052	18.316	16.968	1.00	28.73	B
ATOM	3195	N	GLU	B	116	13.194	19.304	17.749	1.00	28.12	B
ATOM	3196	CA	GLU	B	116	13.861	20.576	17.980	1.00	31.56	B
ATOM	3197	CB	GLU	B	116	13.295	21.648	17.045	1.00	31.98	B
ATOM	3198	CG	GLU	B	116	14.256	22.789	16.788	1.00	40.66	B
ATOM	3199	CD	GLU	B	116	13.627	23.919	15.987	1.00	45.84	B
ATOM	3200	OE1	GLU	B	116	12.929	23.642	14.983	1.00	45.42	B
ATOM	3201	OE2	GLU	B	116	13.837	25.091	16.361	1.00	47.61	B
ATOM	3202	C	GLU	B	116	13.654	21.000	19.426	1.00	29.28	B
ATOM	3203	O	GLU	B	116	12.549	20.909	19.951	1.00	29.19	B
ATOM	3204	N	GLY	B	117	14.723	21.447	20.069	1.00	31.75	B
ATOM	3205	CA	GLY	B	117	14.617	21.884	21.445	1.00	27.56	B
ATOM	3206	C	GLY	B	117	13.843	23.189	21.528	1.00	33.43	B
ATOM	3207	O	GLY	B	117	13.718	23.902	20.528	1.00	28.65	B
ATOM	3208	N	PRO	B	118	13.297	23.527	22.708	1.00	31.86	B
ATOM	3209	CD	PRO	B	118	12.594	24.792	23.003	1.00	32.36	B
ATOM	3210	CA	PRO	B	118	13.413	22.700	23.910	1.00	31.85	B
ATOM	3211	CB	PRO	B	118	13.171	23.707	25.035	1.00	33.45	B
ATOM	3212	CG	PRO	B	118	12.129	24.600	24.441	1.00	30.11	B
ATOM	3213	C	PRO	B	118	12.391	21.558	23.903	1.00	31.09	B
ATOM	3214	O	PRO	B	118	11.193	21.781	23.713	1.00	33.18	B
ATOM	3215	N	SER	B	119	12.886	20.338	24.089	1.00	27.10	B
ATOM	3216	CA	SER	B	119	12.058	19.137	24.130	1.00	26.96	B
ATOM	3217	CB	SER	B	119	11.946	18.493	22.744	1.00	24.46	B
ATOM	3218	OG	SER	B	119	11.198	19.289	21.845	1.00	32.24	B
ATOM	3219	C	SER	B	119	12.750	18.163	25.079	1.00	29.97	B
ATOM	3220	O	SER	B	119	13.983	18.087	25.106	1.00	27.78	B
ATOM	3221	N	LYS	B	120	11.966	17.414	25.847	1.00	26.85	B
ATOM	3222	CA	LYS	B	120	12.530	16.462	26.792	1.00	28.38	B
ATOM	3223	CB	LYS	B	120	12.717	17.138	28.151	1.00	31.21	B
ATOM	3224	CG	LYS	B	120	13.942	18.042	28.200	1.00	43.39	B
ATOM	3225	CD	LYS	B	120	13.820	19.172	29.227	1.00	50.16	B
ATOM	3226	CE	LYS	B	120	13.609	18.649	30.621	1.00	51.00	B
ATOM	3227	NZ	LYS	B	120	12.267	18.012	30.741	1.00	59.68	B
ATOM	3228	C	LYS	B	120	11.706	15.196	26.954	1.00	24.77	B
ATOM	3229	O	LYS	B	120	10.485	15.211	26.827	1.00	25.32	B
ATOM	3230	N	ASN	B	121	12.404	14.104	27.240	1.00	21.77	B
ATOM	3231	CA	ASN	B	121	11.801	12.791	27.432	1.00	21.01	B

ATOM	3232	CB	ASN	B	121	10.948	12.765	28.707	1.00	23.89	B
ATOM	3233	CG	ASN	B	121	11.778	12.972	29.966	1.00	23.76	B
ATOM	3234	OD1	ASN	B	121	12.077	14.097	30.342	1.00	24.77	B
ATOM	3235	ND2	ASN	B	121	12.168	11.879	30.608	1.00	25.97	B
ATOM	3236	C	ASN	B	121	10.980	12.340	26.237	1.00	21.99	B
ATOM	3237	O	ASN	B	121	9.751	12.378	26.251	1.00	16.98	B
ATOM	3238	N	ILE	B	122	11.691	11.898	25.207	1.00	21.03	B
ATOM	3239	CA	ILE	B	122	11.085	11.423	23.974	1.00	22.10	B
ATOM	3240	CB	ILE	B	122	11.516	12.296	22.765	1.00	25.84	B
ATOM	3241	CG2	ILE	B	122	10.677	11.944	21.550	1.00	25.77	B
ATOM	3242	CG1	ILE	B	122	11.389	13.784	23.103	1.00	27.59	B
ATOM	3243	CD1	ILE	B	122	9.977	14.238	23.377	1.00	40.38	B
ATOM	3244	C	ILE	B	122	11.553	9.989	23.716	1.00	19.72	B
ATOM	3245	O	ILE	B	122	12.742	9.689	23.818	1.00	16.73	B
ATOM	3246	N	TRP	B	123	10.610	9.115	23.376	1.00	21.20	B
ATOM	3247	CA	TRP	B	123	10.905	7.711	23.090	1.00	22.94	B
ATOM	3248	CB	TRP	B	123	10.246	6.815	24.158	1.00	21.39	B
ATOM	3249	CG	TRP	B	123	10.584	5.339	24.080	1.00	26.45	B
ATOM	3250	CD2	TRP	B	123	9.884	4.260	24.724	1.00	25.75	B
ATOM	3251	CE2	TRP	B	123	10.580	3.068	24.419	1.00	23.60	B
ATOM	3252	CE3	TRP	B	123	8.740	4.187	25.534	1.00	27.49	B
ATOM	3253	CD1	TRP	B	123	11.640	4.770	23.432	1.00	22.31	B
ATOM	3254	NE1	TRP	B	123	11.646	3.409	23.631	1.00	21.91	B
ATOM	3255	CZ2	TRP	B	123	10.169	1.812	24.893	1.00	25.69	B
ATOM	3256	CZ3	TRP	B	123	8.332	2.932	26.009	1.00	27.42	B
ATOM	3257	CH2	TRP	B	123	9.048	1.766	25.684	1.00	26.44	B
ATOM	3258	C	TRP	B	123	10.386	7.369	21.693	1.00	17.94	B
ATOM	3259	O	TRP	B	123	9.176	7.342	21.457	1.00	22.76	B
ATOM	3260	N	VAL	B	124	11.310	7.148	20.764	1.00	22.92	B
ATOM	3261	CA	VAL	B	124	10.961	6.802	19.385	1.00	18.95	B
ATOM	3262	CB	VAL	B	124	11.803	7.623	18.387	1.00	22.00	B
ATOM	3263	CG1	VAL	B	124	11.400	7.291	16.963	1.00	20.81	B
ATOM	3264	CG2	VAL	B	124	11.600	9.110	18.657	1.00	22.18	B
ATOM	3265	C	VAL	B	124	11.252	5.310	19.269	1.00	21.60	B
ATOM	3266	O	VAL	B	124	12.405	4.883	19.135	1.00	22.39	B
ATOM	3267	N	ASP	B	125	10.185	4.522	19.312	1.00	21.59	B
ATOM	3268	CA	ASP	B	125	10.306	3.073	19.331	1.00	21.01	B
ATOM	3269	CB	ASP	B	125	9.933	2.615	20.745	1.00	22.23	B
ATOM	3270	CG	ASP	B	125	9.969	1.115	20.914	1.00	23.06	B
ATOM	3271	OD1	ASP	B	125	11.075	.563	21.058	1.00	28.95	B
ATOM	3272	OD2	ASP	B	125	8.886	.491	20.901	1.00	23.94	B
ATOM	3273	C	ASP	B	125	9.498	2.293	18.296	1.00	22.66	B
ATOM	3274	O	ASP	B	125	8.384	2.669	17.937	1.00	21.37	B
ATOM	3275	N	HIS	B	126	10.083	1.200	17.823	1.00	21.04	B
ATOM	3276	CA	HIS	B	126	9.446	.319	16.850	1.00	22.51	B
ATOM	3277	CB	HIS	B	126	8.423	-.576	17.565	1.00	21.68	B
ATOM	3278	CG	HIS	B	126	9.038	-1.753	18.260	1.00	25.08	B
ATOM	3279	CD2	HIS	B	126	9.433	-2.959	17.784	1.00	21.64	B
ATOM	3280	ND1	HIS	B	126	9.374	-1.742	19.596	1.00	24.47	B
ATOM	3281	CE1	HIS	B	126	9.948	-2.888	19.913	1.00	25.85	B
ATOM	3282	NE2	HIS	B	126	9.998	-3.643	18.832	1.00	24.73	B
ATOM	3283	C	HIS	B	126	8.801	.969	15.623	1.00	19.31	B
ATOM	3284	O	HIS	B	126	7.660	.676	15.276	1.00	18.48	B
ATOM	3285	N	ASN	B	127	9.544	1.845	14.962	1.00	20.04	B
ATOM	3286	CA	ASN	B	127	9.045	2.512	13.768	1.00	22.87	B
ATOM	3287	CB	ASN	B	127	9.164	4.033	13.916	1.00	20.53	B
ATOM	3288	CG	ASN	B	127	8.410	4.560	15.109	1.00	18.38	B
ATOM	3289	OD1	ASN	B	127	7.185	4.626	15.098	1.00	19.36	B
ATOM	3290	ND2	ASN	B	127	9.139	4.927	16.155	1.00	18.79	B
ATOM	3291	C	ASN	B	127	9.883	2.084	12.575	1.00	25.02	B
ATOM	3292	O	ASN	B	127	10.988	1.568	12.741	1.00	24.96	B
ATOM	3293	N	GLU	B	128	9.351	2.288	11.377	1.00	24.98	B
ATOM	3294	CA	GLU	B	128	10.098	1.996	10.160	1.00	24.28	B
ATOM	3295	CB	GLU	B	128	9.384	.993	9.247	1.00	24.54	B
ATOM	3296	CG	GLU	B	128	10.187	.769	7.962	1.00	26.33	B
ATOM	3297	CD	GLU	B	128	9.679	-.362	7.091	1.00	30.57	B
ATOM	3298	OE1	GLU	B	128	8.710	-1.041	7.480	1.00	30.29	B
ATOM	3299	OE2	GLU	B	128	10.266	-.571	6.011	1.00	31.91	B
ATOM	3300	C	GLU	B	128	10.231	3.334	9.446	1.00	23.76	B

ATOM	3301	O	GLU	B	128	9.231	3.947	9.057	1.00	26.16	B
ATOM	3302	N	LEU	B	129	11.470	3.785	9.288	1.00	25.78	B
ATOM	3303	CA	LEU	B	129	11.749	5.063	8.657	1.00	25.16	B
ATOM	3304	CB	LEU	B	129	12.433	5.987	9.662	1.00	23.67	B
ATOM	3305	CG	LEU	B	129	11.779	6.063	11.042	1.00	26.09	B
ATOM	3306	CD1	LEU	B	129	12.641	6.910	11.961	1.00	28.05	B
ATOM	3307	CD2	LEU	B	129	10.383	6.628	10.926	1.00	24.71	B
ATOM	3308	C	LEU	B	129	12.651	4.875	7.445	1.00	30.52	B
ATOM	3309	O	LEU	B	129	13.720	4.276	7.553	1.00	24.66	B
ATOM	3310	N	TYR	B	130	12.220	5.394	6.298	1.00	28.01	B
ATOM	3311	CA	TYR	B	130	13.007	5.273	5.079	1.00	30.50	B
ATOM	3312	CB	TYR	B	130	12.871	3.864	4.488	1.00	25.90	B
ATOM	3313	CG	TYR	B	130	11.488	3.489	3.981	1.00	31.47	B
ATOM	3314	CD1	TYR	B	130	10.506	2.985	4.847	1.00	31.53	B
ATOM	3315	CE1	TYR	B	130	9.254	2.581	4.362	1.00	29.92	B
ATOM	3316	CD2	TYR	B	130	11.176	3.587	2.627	1.00	27.55	B
ATOM	3317	CE2	TYR	B	130	9.938	3.194	2.139	1.00	27.15	B
ATOM	3318	CZ	TYR	B	130	8.984	2.689	3.003	1.00	33.33	B
ATOM	3319	OH	TYR	B	130	7.765	2.281	2.493	1.00	30.92	B
ATOM	3320	C	TYR	B	130	12.655	6.301	4.007	1.00	29.94	B
ATOM	3321	O	TYR	B	130	11.581	6.889	4.011	1.00	26.77	B
ATOM	3322	N	HIS	B	131	13.599	6.519	3.101	1.00	32.25	B
ATOM	3323	CA	HIS	B	131	13.423	7.437	1.986	1.00	31.20	B
ATOM	3324	CB	HIS	B	131	14.378	8.630	2.099	1.00	30.63	B
ATOM	3325	CG	HIS	B	131	13.992	9.623	3.152	1.00	30.44	B
ATOM	3326	CD2	HIS	B	131	14.740	10.296	4.060	1.00	25.58	B
ATOM	3327	ND1	HIS	B	131	12.702	10.085	3.299	1.00	23.91	B
ATOM	3328	CE1	HIS	B	131	12.672	11.002	4.250	1.00	26.61	B
ATOM	3329	NE2	HIS	B	131	13.895	11.150	4.727	1.00	27.15	B
ATOM	3330	C	HIS	B	131	13.764	6.624	.745	1.00	34.51	B
ATOM	3331	O	HIS	B	131	13.132	5.606	.470	1.00	36.87	B
ATOM	3332	N	SER	B	132	14.780	7.062	.014	1.00	33.61	B
ATOM	3333	CA	SER	B	132	15.214	6.360	-1.189	1.00	36.68	B
ATOM	3334	CB	SER	B	132	14.260	6.653	-2.351	1.00	37.99	B
ATOM	3335	OG	SER	B	132	14.627	5.924	-3.514	1.00	42.27	B
ATOM	3336	C	SER	B	132	16.621	6.806	-1.568	1.00	34.27	B
ATOM	3337	O	SER	B	132	17.014	7.946	-1.318	1.00	33.54	B
ATOM	3338	N	LEU	B	133	17.385	5.894	-2.152	1.00	36.28	B
ATOM	3339	CA	LEU	B	133	18.731	6.218	-2.588	1.00	38.39	B
ATOM	3340	CB	LEU	B	133	19.691	5.061	-2.289	1.00	40.01	B
ATOM	3341	CG	LEU	B	133	20.189	4.940	-.845	1.00	37.28	B
ATOM	3342	CD1	LEU	B	133	21.102	3.739	-.721	1.00	39.53	B
ATOM	3343	CD2	LEU	B	133	20.934	6.201	-.453	1.00	40.11	B
ATOM	3344	C	LEU	B	133	18.703	6.504	-4.088	1.00	41.38	B
ATOM	3345	O	LEU	B	133	19.673	7.002	-4.655	1.00	44.01	B
ATOM	3346	N	ASN	B	134	17.574	6.215	-4.722	1.00	40.74	B
ATOM	3347	CA	ASN	B	134	17.443	6.415	-6.159	1.00	42.28	B
ATOM	3348	CB	ASN	B	134	16.617	5.283	-6.763	1.00	45.25	B
ATOM	3349	CG	ASN	B	134	17.209	3.916	-6.465	1.00	51.31	B
ATOM	3350	OD1	ASN	B	134	18.394	3.663	-6.724	1.00	51.90	B
ATOM	3351	ND2	ASN	B	134	16.390	3.024	-5.911	1.00	55.04	B
ATOM	3352	C	ASN	B	134	16.844	7.758	-6.551	1.00	41.96	B
ATOM	3353	O	ASN	B	134	16.006	7.835	-7.444	1.00	43.08	B
ATOM	3354	N	VAL	B	135	17.279	8.814	-5.875	1.00	39.59	B
ATOM	3355	CA	VAL	B	135	16.814	10.163	-6.160	1.00	34.83	B
ATOM	3356	CB	VAL	B	135	15.624	10.565	-5.254	1.00	37.42	B
ATOM	3357	CG1	VAL	B	135	14.410	9.723	-5.586	1.00	39.01	B
ATOM	3358	CG2	VAL	B	135	15.998	10.387	-3.796	1.00	36.51	B
ATOM	3359	C	VAL	B	135	17.975	11.101	-5.885	1.00	34.41	B
ATOM	3360	O	VAL	B	135	18.983	10.682	-5.320	1.00	33.46	B
ATOM	3361	N	ASP	B	136	17.844	12.360	-6.300	1.00	34.23	B
ATOM	3362	CA	ASP	B	136	18.885	13.355	-6.053	1.00	33.34	B
ATOM	3363	CB	ASP	B	136	18.433	14.740	-6.520	1.00	31.54	B
ATOM	3364	CG	ASP	B	136	18.352	14.856	-8.030	1.00	35.33	B
ATOM	3365	OD1	ASP	B	136	17.863	15.905	-8.503	1.00	38.83	B
ATOM	3366	OD2	ASP	B	136	18.780	13.916	-8.737	1.00	31.69	B
ATOM	3367	C	ASP	B	136	19.118	13.389	-4.546	1.00	36.81	B
ATOM	3368	O	ASP	B	136	18.187	13.168	-3.772	1.00	39.30	B
ATOM	3369	N	LYS	B	137	20.346	13.671	-4.124	1.00	35.61	B

ATOM	3370	CA	LYS	B	137	20.647	13.707	-2.700	1.00	36.20	B
ATOM	3371	CB	LYS	B	137	22.155	13.901	-2.478	1.00	36.21	B
ATOM	3372	CG	LYS	B	137	22.554	13.834	-1.003	1.00	40.73	B
ATOM	3373	CD	LYS	B	137	24.011	14.193	-.737	1.00	40.50	B
ATOM	3374	CE	LYS	B	137	24.973	13.116	-1.169	1.00	40.83	B
ATOM	3375	NZ	LYS	B	137	26.340	13.457	-.674	1.00	39.85	B
ATOM	3376	C	LYS	B	137	19.868	14.769	-1.900	1.00	36.48	B
ATOM	3377	O	LYS	B	137	19.625	14.590	-.709	1.00	34.21	B
ATOM	3378	N	ASP	B	138	19.466	15.865	-2.540	1.00	31.42	B
ATOM	3379	CA	ASP	B	138	18.752	16.921	-1.825	1.00	30.07	B
ATOM	3380	CB	ASP	B	138	19.197	18.302	-2.345	1.00	36.78	B
ATOM	3381	CG	ASP	B	138	18.691	18.601	-3.757	1.00	38.97	B
ATOM	3382	OD1	ASP	B	138	18.182	17.682	-4.431	1.00	42.30	B
ATOM	3383	OD2	ASP	B	138	18.811	19.767	-4.203	1.00	45.75	B
ATOM	3384	C	ASP	B	138	17.230	16.793	-1.911	1.00	29.83	B
ATOM	3385	O	ASP	B	138	16.500	17.634	-1.387	1.00	26.85	B
ATOM	3386	N	TYR	B	139	16.758	15.730	-2.555	1.00	32.56	B
ATOM	3387	CA	TYR	B	139	15.323	15.529	-2.712	1.00	33.42	B
ATOM	3388	CB	TYR	B	139	15.039	14.386	-3.690	1.00	35.61	B
ATOM	3389	CG	TYR	B	139	13.597	14.353	-4.124	1.00	39.30	B
ATOM	3390	CD1	TYR	B	139	13.073	15.375	-4.921	1.00	41.90	B
ATOM	3391	CE1	TYR	B	139	11.732	15.390	-5.292	1.00	45.80	B
ATOM	3392	CD2	TYR	B	139	12.740	13.334	-3.707	1.00	41.29	B
ATOM	3393	CE2	TYR	B	139	11.389	13.337	-4.068	1.00	40.76	B
ATOM	3394	CZ	TYR	B	139	10.892	14.371	-4.860	1.00	48.12	B
ATOM	3395	OH	TYR	B	139	9.556	14.412	-5.208	1.00	49.44	B
ATOM	3396	C	TYR	B	139	14.645	15.239	-1.371	1.00	34.65	B
ATOM	3397	O	TYR	B	139	13.603	15.816	-1.058	1.00	34.48	B
ATOM	3398	N	TYR	B	140	15.227	14.327	-.596	1.00	33.43	B
ATOM	3399	CA	TYR	B	140	14.712	13.977	.729	1.00	30.79	B
ATOM	3400	CB	TYR	B	140	14.483	12.468	.867	1.00	31.48	B
ATOM	3401	CG	TYR	B	140	13.438	11.867	-.048	1.00	27.06	B
ATOM	3402	CD1	TYR	B	140	13.757	10.797	-.884	1.00	25.85	B
ATOM	3403	CE1	TYR	B	140	12.798	10.208	-1.707	1.00	26.23	B
ATOM	3404	CD2	TYR	B	140	12.129	12.339	-.054	1.00	26.14	B
ATOM	3405	CE2	TYR	B	140	11.155	11.756	-.878	1.00	29.24	B
ATOM	3406	CZ	TYR	B	140	11.499	10.692	-1.699	1.00	29.20	B
ATOM	3407	OH	TYR	B	140	10.547	10.120	-2.511	1.00	33.34	B
ATOM	3408	C	TYR	B	140	15.826	14.377	1.695	1.00	34.07	B
ATOM	3409	O	TYR	B	140	16.989	14.498	1.291	1.00	32.42	B
ATOM	3410	N	ASP	B	141	15.487	14.582	2.963	1.00	31.40	B
ATOM	3411	CA	ASP	B	141	16.505	14.946	3.927	1.00	27.73	B
ATOM	3412	CB	ASP	B	141	16.208	16.320	4.537	1.00	28.12	B
ATOM	3413	CG	ASP	B	141	17.422	16.915	5.214	1.00	33.47	B
ATOM	3414	OD1	ASP	B	141	18.530	16.772	4.651	1.00	38.92	B
ATOM	3415	OD2	ASP	B	141	17.284	17.524	6.293	1.00	38.66	B
ATOM	3416	C	ASP	B	141	16.676	13.896	5.031	1.00	30.95	B
ATOM	3417	O	ASP	B	141	16.823	12.711	4.749	1.00	26.12	B
ATOM	3418	N	GLY	B	142	16.639	14.328	6.285	1.00	27.65	B
ATOM	3419	CA	GLY	B	142	16.840	13.399	7.382	1.00	29.23	B
ATOM	3420	C	GLY	B	142	15.752	12.382	7.677	1.00	26.18	B
ATOM	3421	O	GLY	B	142	14.599	12.539	7.283	1.00	28.98	B
ATOM	3422	N	LEU	B	143	16.142	11.317	8.367	1.00	27.20	B
ATOM	3423	CA	LEU	B	143	15.202	10.282	8.771	1.00	27.19	B
ATOM	3424	CB	LEU	B	143	15.814	8.895	8.569	1.00	26.53	B
ATOM	3425	CG	LEU	B	143	15.828	8.431	7.111	1.00	30.29	B
ATOM	3426	CD1	LEU	B	143	16.655	7.163	6.984	1.00	30.68	B
ATOM	3427	CD2	LEU	B	143	14.394	8.193	6.629	1.00	27.86	B
ATOM	3428	C	LEU	B	143	14.874	10.525	10.252	1.00	27.98	B
ATOM	3429	O	LEU	B	143	13.733	10.352	10.684	1.00	27.66	B
ATOM	3430	N	PHE	B	144	15.885	10.932	11.014	1.00	25.84	B
ATOM	3431	CA	PHE	B	144	15.723	11.236	12.440	1.00	28.51	B
ATOM	3432	CB	PHE	B	144	15.893	9.981	13.304	1.00	28.18	B
ATOM	3433	CG	PHE	B	144	15.786	10.242	14.790	1.00	29.28	B
ATOM	3434	CD1	PHE	B	144	16.867	10.011	15.629	1.00	26.74	B
ATOM	3435	CD2	PHE	B	144	14.598	10.698	15.346	1.00	28.15	B
ATOM	3436	CE1	PHE	B	144	16.768	10.227	17.004	1.00	27.28	B
ATOM	3437	CE2	PHE	B	144	14.488	10.917	16.722	1.00	30.36	B
ATOM	3438	CZ	PHE	B	144	15.573	10.681	17.551	1.00	27.31	B

ATOM	3439	C	PHE	B	144	16.775	12.258	12.828	1.00	26.95	B
ATOM	3440	O	PHE	B	144	17.914	11.908	13.129	1.00	28.13	B
ATOM	3441	N	ASP	B	145	16.389	13.526	12.795	1.00	28.28	B
ATOM	3442	CA	ASP	B	145	17.301	14.605	13.135	1.00	27.21	B
ATOM	3443	CB	ASP	B	145	17.363	15.649	12.007	1.00	28.42	B
ATOM	3444	CG	ASP	B	145	17.942	15.090	10.721	1.00	29.32	B
ATOM	3445	OD1	ASP	B	145	18.663	14.071	10.775	1.00	30.25	B
ATOM	3446	OD2	ASP	B	145	17.687	15.677	9.650	1.00	34.16	B
ATOM	3447	C	ASP	B	145	16.876	15.278	14.428	1.00	30.21	B
ATOM	3448	O	ASP	B	145	15.693	15.354	14.747	1.00	29.37	B
ATOM	3449	N	VAL	B	146	17.862	15.772	15.163	1.00	30.16	B
ATOM	3450	CA	VAL	B	146	17.625	16.433	16.430	1.00	29.53	B
ATOM	3451	CB	VAL	B	146	18.011	15.511	17.609	1.00	28.68	B
ATOM	3452	CG1	VAL	B	146	17.618	16.152	18.920	1.00	30.18	B
ATOM	3453	CG2	VAL	B	146	17.343	14.157	17.456	1.00	26.99	B
ATOM	3454	C	VAL	B	146	18.510	17.665	16.471	1.00	31.71	B
ATOM	3455	O	VAL	B	146	19.697	17.578	16.172	1.00	33.00	B
ATOM	3456	N	LYS	B	147	17.938	18.809	16.834	1.00	31.70	B
ATOM	3457	CA	LYS	B	147	18.717	20.033	16.907	1.00	34.22	B
ATOM	3458	CB	LYS	B	147	18.472	20.918	15.680	1.00	35.14	B
ATOM	3459	CG	LYS	B	147	17.013	21.281	15.452	1.00	42.55	B
ATOM	3460	CD	LYS	B	147	16.849	22.370	14.397	1.00	50.31	B
ATOM	3461	CE	LYS	B	147	17.411	21.949	13.046	1.00	53.42	B
ATOM	3462	NZ	LYS	B	147	16.697	20.754	12.504	1.00	61.09	B
ATOM	3463	C	LYS	B	147	18.407	20.812	18.172	1.00	34.27	B
ATOM	3464	O	LYS	B	147	17.369	20.621	18.811	1.00	32.11	B
ATOM	3465	N	ARG	B	148	19.343	21.677	18.536	1.00	32.91	B
ATOM	3466	CA	ARG	B	148	19.220	22.511	19.714	1.00	35.12	B
ATOM	3467	CB	ARG	B	148	18.042	23.463	19.551	1.00	39.92	B
ATOM	3468	CG	ARG	B	148	18.265	24.778	20.266	1.00	55.90	B
ATOM	3469	CD	ARG	B	148	17.391	25.865	19.675	1.00	62.74	B
ATOM	3470	NE	ARG	B	148	17.351	25.778	18.219	1.00	67.89	B
ATOM	3471	CZ	ARG	B	148	16.214	25.694	17.539	1.00	75.54	B
ATOM	3472	NH1	ARG	B	148	16.214	25.618	16.208	1.00	78.49	B
ATOM	3473	NH2	ARG	B	148	15.063	25.686	18.208	1.00	78.93	B
ATOM	3474	C	ARG	B	148	19.118	21.752	21.036	1.00	33.09	B
ATOM	3475	O	ARG	B	148	19.680	20.664	21.181	1.00	32.62	B
ATOM	3476	N	ASP	B	149	18.399	22.323	21.999	1.00	31.57	B
ATOM	3477	CA	ASP	B	149	18.296	21.720	23.322	1.00	34.42	B
ATOM	3478	CB	ASP	B	149	18.140	22.811	24.396	1.00	36.47	B
ATOM	3479	CG	ASP	B	149	17.077	23.842	24.054	1.00	37.71	B
ATOM	3480	OD1	ASP	B	149	16.679	24.597	24.963	1.00	39.17	B
ATOM	3481	OD2	ASP	B	149	16.646	23.917	22.883	1.00	39.15	B
ATOM	3482	C	ASP	B	149	17.241	20.647	23.544	1.00	34.18	B
ATOM	3483	O	ASP	B	149	16.236	20.879	24.215	1.00	33.58	B
ATOM	3484	N	ALA	B	150	17.487	19.466	22.990	1.00	31.44	B
ATOM	3485	CA	ALA	B	150	16.576	18.347	23.145	1.00	31.03	B
ATOM	3486	CB	ALA	B	150	16.240	17.746	21.790	1.00	28.78	B
ATOM	3487	C	ALA	B	150	17.354	17.359	23.983	1.00	33.40	B
ATOM	3488	O	ALA	B	150	18.526	17.111	23.704	1.00	36.62	B
ATOM	3489	N	GLU	B	151	16.730	16.806	25.016	1.00	33.08	B
ATOM	3490	CA	GLU	B	151	17.429	15.854	25.878	1.00	32.03	B
ATOM	3491	CB	GLU	B	151	18.114	16.606	27.018	1.00	32.94	B
ATOM	3492	CG	GLU	B	151	17.236	17.612	27.731	1.00	40.65	B
ATOM	3493	CD	GLU	B	151	18.051	18.688	28.433	1.00	42.03	B
ATOM	3494	OE1	GLU	B	151	18.976	18.326	29.192	1.00	38.31	B
ATOM	3495	OE2	GLU	B	151	17.759	19.887	28.220	1.00	42.69	B
ATOM	3496	C	GLU	B	151	16.574	14.724	26.441	1.00	27.10	B
ATOM	3497	O	GLU	B	151	15.342	14.799	26.448	1.00	25.88	B
ATOM	3498	N	TYR	B	152	17.254	13.680	26.913	1.00	25.89	B
ATOM	3499	CA	TYR	B	152	16.603	12.497	27.471	1.00	22.83	B
ATOM	3500	CB	TYR	B	152	15.727	12.892	28.664	1.00	27.84	B
ATOM	3501	CG	TYR	B	152	16.512	13.558	29.762	1.00	26.93	B
ATOM	3502	CD1	TYR	B	152	17.506	12.858	30.449	1.00	34.41	B
ATOM	3503	CE1	TYR	B	152	18.279	13.476	31.431	1.00	33.94	B
ATOM	3504	CD2	TYR	B	152	16.302	14.899	30.086	1.00	30.75	B
ATOM	3505	CE2	TYR	B	152	17.067	15.532	31.063	1.00	31.89	B
ATOM	3506	CZ	TYR	B	152	18.056	14.815	31.729	1.00	37.79	B
ATOM	3507	OH	TYR	B	152	18.842	15.440	32.670	1.00	41.03	B

ATOM	3508	C	TYR	B	152	15.771	11.847	26.378	1.00	21.99	B
ATOM	3509	O	TYR	B	152	14.548	11.793	26.454	1.00	21.55	B
ATOM	3510	N	ILE	B	153	16.463	11.354	25.358	1.00	19.71	B
ATOM	3511	CA	ILE	B	153	15.831	10.715	24.216	1.00	22.12	B
ATOM	3512	CB	ILE	B	153	16.120	11.514	22.925	1.00	23.41	B
ATOM	3513	CG2	ILE	B	153	15.496	10.823	21.724	1.00	19.67	B
ATOM	3514	CG1	ILE	B	153	15.595	12.940	23.067	1.00	26.30	B
ATOM	3515	CD1	ILE	B	153	16.027	13.859	21.941	1.00	29.98	B
ATOM	3516	C	ILE	B	153	16.329	9.288	23.995	1.00	22.99	B
ATOM	3517	O	ILE	B	153	17.530	9.027	24.031	1.00	26.23	B
ATOM	3518	N	THR	B	154	15.404	8.366	23.772	1.00	22.59	B
ATOM	3519	CA	THR	B	154	15.780	6.987	23.491	1.00	21.35	B
ATOM	3520	CB	THR	B	154	15.268	6.008	24.568	1.00	21.64	B
ATOM	3521	OG1	THR	B	154	15.926	6.281	25.810	1.00	21.16	B
ATOM	3522	CG2	THR	B	154	15.546	4.566	24.155	1.00	18.52	B
ATOM	3523	C	THR	B	154	15.196	6.609	22.134	1.00	22.47	B
ATOM	3524	O	THR	B	154	13.996	6.768	21.887	1.00	22.69	B
ATOM	3525	N	PHE	B	155	16.072	6.136	21.253	1.00	23.61	B
ATOM	3526	CA	PHE	B	155	15.718	5.722	19.896	1.00	22.37	B
ATOM	3527	CB	PHE	B	155	16.642	6.431	18.902	1.00	21.52	B
ATOM	3528	CG	PHE	B	155	16.241	6.274	17.466	1.00	22.06	B
ATOM	3529	CD1	PHE	B	155	15.190	7.019	16.935	1.00	21.94	B
ATOM	3530	CD2	PHE	B	155	16.932	5.400	16.631	1.00	21.25	B
ATOM	3531	CE1	PHE	B	155	14.836	6.897	15.582	1.00	25.50	B
ATOM	3532	CE2	PHE	B	155	16.585	5.272	15.284	1.00	22.90	B
ATOM	3533	CZ	PHE	B	155	15.538	6.021	14.757	1.00	22.24	B
ATOM	3534	C	PHE	B	155	15.990	4.219	19.900	1.00	25.34	B
ATOM	3535	O	PHE	B	155	17.147	3.796	19.913	1.00	22.32	B
ATOM	3536	N	SER	B	156	14.933	3.415	19.879	1.00	24.39	B
ATOM	3537	CA	SER	B	156	15.101	1.968	19.952	1.00	22.59	B
ATOM	3538	CB	SER	B	156	14.917	1.520	21.406	1.00	27.69	B
ATOM	3539	OG	SER	B	156	13.587	1.778	21.842	1.00	22.30	B
ATOM	3540	C	SER	B	156	14.182	1.122	19.075	1.00	23.84	B
ATOM	3541	O	SER	B	156	13.059	1.509	18.763	1.00	24.27	B
ATOM	3542	N	TRP	B	157	14.686	-.054	18.709	1.00	24.44	B
ATOM	3543	CA	TRP	B	157	13.954	-1.030	17.904	1.00	24.03	B
ATOM	3544	CB	TRP	B	157	12.834	-1.658	18.742	1.00	21.20	B
ATOM	3545	CG	TRP	B	157	13.319	-2.359	19.980	1.00	25.16	B
ATOM	3546	CD2	TRP	B	157	13.911	-3.668	20.054	1.00	24.13	B
ATOM	3547	CE2	TRP	B	157	14.219	-3.912	21.415	1.00	26.18	B
ATOM	3548	CE3	TRP	B	157	14.213	-4.657	19.101	1.00	23.08	B
ATOM	3549	CD1	TRP	B	157	13.295	-1.879	21.261	1.00	24.61	B
ATOM	3550	NE1	TRP	B	157	13.834	-2.806	22.127	1.00	25.54	B
ATOM	3551	CZ2	TRP	B	157	14.814	-5.106	21.848	1.00	23.41	B
ATOM	3552	CZ3	TRP	B	157	14.805	-5.846	19.532	1.00	23.05	B
ATOM	3553	CH2	TRP	B	157	15.098	-6.058	20.896	1.00	24.40	B
ATOM	3554	C	TRP	B	157	13.382	-.501	16.592	1.00	21.15	B
ATOM	3555	O	TRP	B	157	12.366	-.993	16.096	1.00	19.86	B
ATOM	3556	N	ASN	B	158	14.053	.492	16.021	1.00	23.66	B
ATOM	3557	CA	ASN	B	158	13.618	1.072	14.764	1.00	24.50	B
ATOM	3558	CB	ASN	B	158	13.892	2.576	14.762	1.00	22.46	B
ATOM	3559	CG	ASN	B	158	13.157	3.301	15.867	1.00	21.47	B
ATOM	3560	OD1	ASN	B	158	11.929	3.385	15.852	1.00	23.21	B
ATOM	3561	ND2	ASN	B	158	13.901	3.822	16.834	1.00	16.59	B
ATOM	3562	C	ASN	B	158	14.320	.425	13.569	1.00	24.50	B
ATOM	3563	O	ASN	B	158	15.435	-.076	13.681	1.00	25.75	B
ATOM	3564	N	TYR	B	159	13.643	.437	12.429	1.00	24.72	B
ATOM	3565	CA	TYR	B	159	14.191	-.100	11.188	1.00	24.40	B
ATOM	3566	CB	TYR	B	159	13.219	-1.114	10.571	1.00	25.95	B
ATOM	3567	CG	TYR	B	159	13.660	-1.699	9.243	1.00	26.77	B
ATOM	3568	CD1	TYR	B	159	15.013	-1.828	8.928	1.00	27.89	B
ATOM	3569	CE1	TYR	B	159	15.427	-2.385	7.711	1.00	30.54	B
ATOM	3570	CD2	TYR	B	159	12.722	-2.145	8.313	1.00	29.43	B
ATOM	3571	CE2	TYR	B	159	13.121	-2.712	7.093	1.00	32.40	B
ATOM	3572	CZ	TYR	B	159	14.474	-2.824	6.800	1.00	32.49	B
ATOM	3573	OH	TYR	B	159	14.872	-3.364	5.602	1.00	38.12	B
ATOM	3574	C	TYR	B	159	14.379	1.115	10.275	1.00	27.50	B
ATOM	3575	O	TYR	B	159	13.430	1.590	9.645	1.00	28.14	B
ATOM	3576	N	VAL	B	160	15.609	1.621	10.238	1.00	25.31	B

ATOM	3577	CA	VAL	B	160	15.962	2.794	9.444	1.00	25.30	B
ATOM	3578	CB	VAL	B	160	16.804	3.762	10.294	1.00	24.83	B
ATOM	3579	CG1	VAL	B	160	16.974	5.089	9.571	1.00	25.52	B
ATOM	3580	CG2	VAL	B	160	16.127	3.967	11.658	1.00	27.11	B
ATOM	3581	C	VAL	B	160	16.755	2.378	8.206	1.00	28.87	B
ATOM	3582	O	VAL	B	160	17.833	1.791	8.323	1.00	29.01	B
ATOM	3583	N	HIS	B	161	16.246	2.703	7.021	1.00	27.14	B
ATOM	3584	CA	HIS	B	161	16.937	2.287	5.804	1.00	29.52	B
ATOM	3585	CB	HIS	B	161	16.557	.829	5.504	1.00	26.41	B
ATOM	3586	CG	HIS	B	161	15.092	.633	5.259	1.00	25.28	B
ATOM	3587	CD2	HIS	B	161	14.068	.397	6.115	1.00	24.78	B
ATOM	3588	ND1	HIS	B	161	14.526	.738	4.008	1.00	25.11	B
ATOM	3589	CE1	HIS	B	161	13.218	.573	4.101	1.00	22.75	B
ATOM	3590	NE2	HIS	B	161	12.914	.365	5.370	1.00	25.64	B
ATOM	3591	C	HIS	B	161	16.674	3.136	4.561	1.00	33.60	B
ATOM	3592	O	HIS	B	161	15.725	3.921	4.508	1.00	31.21	B
ATOM	3593	N	ASP	B	162	17.532	2.963	3.558	1.00	32.95	B
ATOM	3594	CA	ASP	B	162	17.398	3.661	2.286	1.00	31.36	B
ATOM	3595	CB	ASP	B	162	16.177	3.106	1.547	1.00	30.99	B
ATOM	3596	CG	ASP	B	162	16.383	1.664	1.104	1.00	37.98	B
ATOM	3597	OD1	ASP	B	162	17.135	1.455	.127	1.00	38.71	B
ATOM	3598	OD2	ASP	B	162	15.825	.737	1.736	1.00	35.59	B
ATOM	3599	C	ASP	B	162	17.328	5.181	2.377	1.00	30.70	B
ATOM	3600	O	ASP	B	162	16.266	5.780	2.223	1.00	32.71	B
ATOM	3601	N	GLY	B	163	18.474	5.802	2.627	1.00	29.15	B
ATOM	3602	CA	GLY	B	163	18.522	7.248	2.714	1.00	33.91	B
ATOM	3603	C	GLY	B	163	19.940	7.755	2.583	1.00	31.94	B
ATOM	3604	O	GLY	B	163	20.880	7.059	2.979	1.00	31.66	B
ATOM	3605	N	TRP	B	164	20.098	8.956	2.025	1.00	31.72	B
ATOM	3606	CA	TRP	B	164	21.420	9.559	1.855	1.00	31.47	B
ATOM	3607	CB	TRP	B	164	21.382	10.686	.815	1.00	31.97	B
ATOM	3608	CG	TRP	B	164	21.352	10.225	-.605	1.00	33.83	B
ATOM	3609	CD2	TRP	B	164	22.474	9.820	-1.395	1.00	36.91	B
ATOM	3610	CE2	TRP	B	164	21.976	9.427	-2.660	1.00	37.38	B
ATOM	3611	CE3	TRP	B	164	23.853	9.749	-1.159	1.00	37.32	B
ATOM	3612	CD1	TRP	B	164	20.251	10.069	-1.396	1.00	35.81	B
ATOM	3613	NE1	TRP	B	164	20.616	9.590	-2.633	1.00	37.69	B
ATOM	3614	CZ2	TRP	B	164	22.811	8.968	-3.687	1.00	37.42	B
ATOM	3615	CZ3	TRP	B	164	24.686	9.291	-2.183	1.00	40.59	B
ATOM	3616	CH2	TRP	B	164	24.158	8.907	-3.430	1.00	39.35	B
ATOM	3617	C	TRP	B	164	21.956	10.134	3.159	1.00	34.76	B
ATOM	3618	O	TRP	B	164	23.127	9.959	3.490	1.00	37.96	B
ATOM	3619	N	LYS	B	165	21.089	10.828	3.891	1.00	37.05	B
ATOM	3620	CA	LYS	B	165	21.459	11.463	5.163	1.00	35.52	B
ATOM	3621	CB	LYS	B	165	21.281	12.978	5.033	1.00	34.96	B
ATOM	3622	CG	LYS	B	165	22.130	13.594	3.913	1.00	33.83	B
ATOM	3623	CD	LYS	B	165	21.504	14.871	3.361	1.00	31.98	B
ATOM	3624	CE	LYS	B	165	20.314	14.548	2.458	1.00	29.92	B
ATOM	3625	NZ	LYS	B	165	19.562	15.768	2.039	1.00	30.47	B
ATOM	3626	C	LYS	B	165	20.541	10.908	6.243	1.00	36.88	B
ATOM	3627	O	LYS	B	165	19.396	11.326	6.364	1.00	39.21	B
ATOM	3628	N	SER	B	166	21.050	9.976	7.042	1.00	37.08	B
ATOM	3629	CA	SER	B	166	20.231	9.332	8.056	1.00	34.14	B
ATOM	3630	CB	SER	B	166	20.884	8.013	8.477	1.00	34.27	B
ATOM	3631	OG	SER	B	166	19.983	7.252	9.258	1.00	39.49	B
ATOM	3632	C	SER	B	166	19.853	10.126	9.301	1.00	31.53	B
ATOM	3633	O	SER	B	166	18.685	10.479	9.487	1.00	28.05	B
ATOM	3634	N	MET	B	167	20.830	10.400	10.158	1.00	29.92	B
ATOM	3635	CA	MET	B	167	20.549	11.104	11.394	1.00	31.03	B
ATOM	3636	CB	MET	B	167	20.486	10.100	12.548	1.00	29.73	B
ATOM	3637	CG	MET	B	167	19.667	8.860	12.227	1.00	29.66	B
ATOM	3638	SD	MET	B	167	19.664	7.660	13.557	1.00	34.83	B
ATOM	3639	CE	MET	B	167	21.174	6.740	13.203	1.00	32.93	B
ATOM	3640	C	MET	B	167	21.555	12.189	11.733	1.00	31.53	B
ATOM	3641	O	MET	B	167	22.748	11.922	11.874	1.00	32.87	B
ATOM	3642	N	LEU	B	168	21.054	13.410	11.889	1.00	30.22	B
ATOM	3643	CA	LEU	B	168	21.890	14.553	12.220	1.00	31.02	B
ATOM	3644	CB	LEU	B	168	21.668	15.679	11.200	1.00	32.82	B
ATOM	3645	CG	LEU	B	168	22.535	16.937	11.316	1.00	35.28	B

ATOM	3646	CD1	LEU	B	168	23.958	16.605	10.915	1.00	39.31	B
ATOM	3647	CD2	LEU	B	168	21.991	18.040	10.397	1.00	35.27	B
ATOM	3648	C	LEU	B	168	21.532	15.055	13.613	1.00	31.05	B
ATOM	3649	O	LEU	B	168	20.415	15.509	13.843	1.00	33.62	B
ATOM	3650	N	MET	B	169	22.479	14.958	14.538	1.00	31.22	B
ATOM	3651	CA	MET	B	169	22.273	15.420	15.902	1.00	30.07	B
ATOM	3652	CB	MET	B	169	22.768	14.364	16.900	1.00	29.41	B
ATOM	3653	CG	MET	B	169	22.321	12.926	16.615	1.00	33.31	B
ATOM	3654	SD	MET	B	169	20.547	12.596	16.780	1.00	41.44	B
ATOM	3655	CE	MET	B	169	20.139	12.232	15.114	1.00	34.10	B
ATOM	3656	C	MET	B	169	23.110	16.695	16.018	1.00	32.14	B
ATOM	3657	O	MET	B	169	24.330	16.635	16.146	1.00	34.47	B
ATOM	3658	N	GLY	B	170	22.454	17.848	15.959	1.00	32.20	B
ATOM	3659	CA	GLY	B	170	23.163	19.114	16.015	1.00	32.55	B
ATOM	3660	C	GLY	B	170	23.205	19.668	14.600	1.00	34.56	B
ATOM	3661	O	GLY	B	170	23.871	19.108	13.732	1.00	36.21	B
ATOM	3662	N	SER	B	171	22.487	20.762	14.370	1.00	38.57	B
ATOM	3663	CA	SER	B	171	22.388	21.397	13.053	1.00	40.20	B
ATOM	3664	CB	SER	B	171	21.369	22.539	13.105	1.00	42.81	B
ATOM	3665	OG	SER	B	171	21.691	23.461	14.140	1.00	44.13	B
ATOM	3666	C	SER	B	171	23.684	21.932	12.456	1.00	43.17	B
ATOM	3667	O	SER	B	171	23.856	21.913	11.237	1.00	42.37	B
ATOM	3668	N	SER	B	172	24.588	22.411	13.306	1.00	42.08	B
ATOM	3669	CA	SER	B	172	25.859	22.961	12.830	1.00	42.34	B
ATOM	3670	CB	SER	B	172	25.676	24.421	12.437	1.00	40.60	B
ATOM	3671	OG	SER	B	172	25.413	25.200	13.595	1.00	42.86	B
ATOM	3672	C	SER	B	172	26.897	22.883	13.939	1.00	41.95	B
ATOM	3673	O	SER	B	172	26.562	22.565	15.085	1.00	39.78	B
ATOM	3674	N	ASP	B	173	28.150	23.189	13.609	1.00	41.95	B
ATOM	3675	CA	ASP	B	173	29.213	23.145	14.605	1.00	41.15	B
ATOM	3676	CB	ASP	B	173	30.591	23.336	13.950	1.00	41.54	B
ATOM	3677	CG	ASP	B	173	31.088	22.079	13.240	1.00	45.76	B
ATOM	3678	OD1	ASP	B	173	30.500	20.990	13.445	1.00	46.48	B
ATOM	3679	OD2	ASP	B	173	32.083	22.172	12.484	1.00	48.79	B
ATOM	3680	C	ASP	B	173	29.002	24.195	15.693	1.00	38.82	B
ATOM	3681	O	ASP	B	173	29.797	24.294	16.627	1.00	41.00	B
ATOM	3682	N	SER	B	174	27.928	24.972	15.581	1.00	41.15	B
ATOM	3683	CA	SER	B	174	27.630	25.998	16.580	1.00	44.12	B
ATOM	3684	CB	SER	B	174	27.464	27.372	15.911	1.00	45.42	B
ATOM	3685	OG	SER	B	174	26.378	27.375	14.995	1.00	50.32	B
ATOM	3686	C	SER	B	174	26.375	25.668	17.406	1.00	46.38	B
ATOM	3687	O	SER	B	174	25.996	26.435	18.302	1.00	44.84	B
ATOM	3688	N	ASP	B	175	25.736	24.536	17.103	1.00	44.82	B
ATOM	3689	CA	ASP	B	175	24.541	24.103	17.837	1.00	44.13	B
ATOM	3690	CB	ASP	B	175	23.708	23.144	16.984	1.00	40.45	B
ATOM	3691	CG	ASP	B	175	22.401	22.746	17.661	1.00	43.36	B
ATOM	3692	OD1	ASP	B	175	21.583	22.035	17.033	1.00	37.84	B
ATOM	3693	OD2	ASP	B	175	22.196	23.151	18.830	1.00	42.36	B
ATOM	3694	C	ASP	B	175	25.038	23.394	19.090	1.00	45.05	B
ATOM	3695	O	ASP	B	175	24.896	22.174	19.243	1.00	46.98	B
ATOM	3696	N	ASN	B	176	25.626	24.178	19.984	1.00	49.38	B
ATOM	3697	CA	ASN	B	176	26.215	23.652	21.205	1.00	51.25	B
ATOM	3698	CB	ASN	B	176	27.373	24.554	21.640	1.00	56.02	B
ATOM	3699	CG	ASN	B	176	26.892	25.859	22.262	1.00	61.89	B
ATOM	3700	OD1	ASN	B	176	25.993	26.529	21.727	1.00	63.33	B
ATOM	3701	ND2	ASN	B	176	27.485	26.227	23.402	1.00	65.21	B
ATOM	3702	C	ASN	B	176	25.267	23.466	22.380	1.00	52.14	B
ATOM	3703	O	ASN	B	176	24.965	24.412	23.115	1.00	51.18	B
ATOM	3704	N	TYR	B	177	24.785	22.242	22.547	1.00	49.95	B
ATOM	3705	CA	TYR	B	177	23.919	21.927	23.670	1.00	49.76	B
ATOM	3706	CB	TYR	B	177	22.437	22.115	23.356	1.00	54.57	B
ATOM	3707	CG	TYR	B	177	21.613	22.057	24.626	1.00	62.59	B
ATOM	3708	CD1	TYR	B	177	21.523	23.166	25.472	1.00	66.78	B
ATOM	3709	CE1	TYR	B	177	20.830	23.096	26.700	1.00	69.15	B
ATOM	3710	CD2	TYR	B	177	20.991	20.867	25.029	1.00	66.42	B
ATOM	3711	CE2	TYR	B	177	20.299	20.780	26.249	1.00	67.80	B
ATOM	3712	CZ	TYR	B	177	20.221	21.897	27.080	1.00	69.92	B
ATOM	3713	OH	TYR	B	177	19.539	21.814	28.285	1.00	66.92	B
ATOM	3714	C	TYR	B	177	24.188	20.479	23.986	1.00	44.38	B

ATOM	3715	O	TYR	B	177	24.529	19.695	23.102	1.00	43.40	B
ATOM	3716	N	ASN	B	178	24.031	20.124	25.248	1.00	40.25	B
ATOM	3717	CA	ASN	B	178	24.315	18.768	25.673	1.00	37.82	B
ATOM	3718	CB	ASN	B	178	24.737	18.777	27.137	1.00	40.08	B
ATOM	3719	CG	ASN	B	178	25.471	17.527	27.525	1.00	45.68	B
ATOM	3720	OD1	ASN	B	178	26.517	17.204	26.953	1.00	51.91	B
ATOM	3721	ND2	ASN	B	178	24.933	16.803	28.495	1.00	49.70	B
ATOM	3722	C	ASN	B	178	23.172	17.788	25.470	1.00	36.89	B
ATOM	3723	O	ASN	B	178	22.519	17.363	26.428	1.00	39.91	B
ATOM	3724	N	ARG	B	179	22.932	17.423	24.220	1.00	33.16	B
ATOM	3725	CA	ARG	B	179	21.883	16.478	23.907	1.00	31.15	B
ATOM	3726	CB	ARG	B	179	21.719	16.387	22.389	1.00	31.48	B
ATOM	3727	CG	ARG	B	179	21.110	17.645	21.756	1.00	29.76	B
ATOM	3728	CD	ARG	B	179	21.170	17.603	20.238	1.00	31.75	B
ATOM	3729	NE	ARG	B	179	22.510	17.921	19.740	1.00	31.79	B
ATOM	3730	CZ	ARG	B	179	22.977	19.157	19.574	1.00	34.10	B
ATOM	3731	NH1	ARG	B	179	24.211	19.349	19.122	1.00	34.44	B
ATOM	3732	NH2	ARG	B	179	22.208	20.204	19.839	1.00	28.22	B
ATOM	3733	C	ARG	B	179	22.273	15.119	24.505	1.00	33.58	B
ATOM	3734	O	ARG	B	179	23.446	14.737	24.488	1.00	32.77	B
ATOM	3735	N	THR	B	180	21.289	14.406	25.047	1.00	31.35	B
ATOM	3736	CA	THR	B	180	21.502	13.089	25.654	1.00	27.82	B
ATOM	3737	CB	THR	B	180	21.158	13.120	27.159	1.00	28.42	B
ATOM	3738	OG1	THR	B	180	20.020	13.971	27.374	1.00	24.23	B
ATOM	3739	CG2	THR	B	180	22.342	13.641	27.967	1.00	26.48	B
ATOM	3740	C	THR	B	180	20.600	12.087	24.943	1.00	28.40	B
ATOM	3741	O	THR	B	180	19.381	12.093	25.129	1.00	28.59	B
ATOM	3742	N	ILE	B	181	21.204	11.218	24.139	1.00	27.82	B
ATOM	3743	CA	ILE	B	181	20.442	10.252	23.355	1.00	26.54	B
ATOM	3744	CB	ILE	B	181	20.404	10.674	21.869	1.00	27.71	B
ATOM	3745	CG2	ILE	B	181	19.465	9.769	21.083	1.00	27.40	B
ATOM	3746	CG1	ILE	B	181	19.939	12.120	21.750	1.00	27.80	B
ATOM	3747	CD1	ILE	B	181	19.910	12.628	20.325	1.00	33.45	B
ATOM	3748	C	ILE	B	181	20.990	8.838	23.408	1.00	26.88	B
ATOM	3749	O	ILE	B	181	22.199	8.626	23.297	1.00	27.18	B
ATOM	3750	N	THR	B	182	20.085	7.873	23.555	1.00	26.97	B
ATOM	3751	CA	THR	B	182	20.450	6.464	23.592	1.00	23.84	B
ATOM	3752	CB	THR	B	182	19.831	5.729	24.806	1.00	23.89	B
ATOM	3753	OG1	THR	B	182	20.314	6.298	26.029	1.00	21.77	B
ATOM	3754	CG2	THR	B	182	20.187	4.249	24.748	1.00	20.36	B
ATOM	3755	C	THR	B	182	19.906	5.802	22.338	1.00	26.87	B
ATOM	3756	O	THR	B	182	18.727	5.963	22.014	1.00	26.85	B
ATOM	3757	N	PHE	B	183	20.764	5.072	21.631	1.00	24.65	B
ATOM	3758	CA	PHE	B	183	20.369	4.350	20.422	1.00	23.79	B
ATOM	3759	CB	PHE	B	183	21.231	4.733	19.211	1.00	27.71	B
ATOM	3760	CG	PHE	B	183	21.168	6.183	18.817	1.00	24.86	B
ATOM	3761	CD1	PHE	B	183	21.893	7.143	19.509	1.00	26.62	B
ATOM	3762	CD2	PHE	B	183	20.430	6.579	17.705	1.00	30.81	B
ATOM	3763	CE1	PHE	B	183	21.891	8.475	19.098	1.00	26.74	B
ATOM	3764	CE2	PHE	B	183	20.421	7.909	17.288	1.00	24.89	B
ATOM	3765	CZ	PHE	B	183	21.153	8.857	17.984	1.00	26.63	B
ATOM	3766	C	PHE	B	183	20.615	2.859	20.671	1.00	29.44	B
ATOM	3767	O	PHE	B	183	21.766	2.453	20.824	1.00	30.26	B
ATOM	3768	N	HIS	B	184	19.571	2.036	20.708	1.00	26.41	B
ATOM	3769	CA	HIS	B	184	19.804	.613	20.915	1.00	25.38	B
ATOM	3770	CB	HIS	B	184	19.844	.285	22.421	1.00	24.50	B
ATOM	3771	CG	HIS	B	184	18.502	.276	23.088	1.00	24.48	B
ATOM	3772	CD2	HIS	B	184	17.831	1.243	23.760	1.00	23.10	B
ATOM	3773	ND1	HIS	B	184	17.696	-.841	23.118	1.00	23.49	B
ATOM	3774	CE1	HIS	B	184	16.587	-.562	23.781	1.00	28.59	B
ATOM	3775	NE2	HIS	B	184	16.643	.695	24.181	1.00	25.46	B
ATOM	3776	C	HIS	B	184	18.805	-.279	20.192	1.00	26.94	B
ATOM	3777	O	HIS	B	184	17.660	.106	19.960	1.00	28.14	B
ATOM	3778	N	HIS	B	185	19.266	-1.473	19.833	1.00	24.71	B
ATOM	3779	CA	HIS	B	185	18.473	-2.469	19.130	1.00	24.30	B
ATOM	3780	CB	HIS	B	185	17.449	-3.105	20.078	1.00	26.70	B
ATOM	3781	CG	HIS	B	185	18.078	-3.901	21.183	1.00	29.43	B
ATOM	3782	CD2	HIS	B	185	18.363	-5.222	21.279	1.00	25.48	B
ATOM	3783	ND1	HIS	B	185	18.567	-3.321	22.336	1.00	26.80	B

ATOM	3784	CE1	HIS	B	185	19.126	-4.249	23.091	1.00	27.00	B
ATOM	3785	NE2	HIS	B	185	19.016	-5.411	22.473	1.00	26.66	B
ATOM	3786	C	HIS	B	185	17.800	-1.972	17.857	1.00	26.05	B
ATOM	3787	O	HIS	B	185	16.712	-2.418	17.496	1.00	26.88	B
ATOM	3788	N	ASN	B	186	18.471	-1.057	17.166	1.00	25.31	B
ATOM	3789	CA	ASN	B	186	17.959	-.525	15.910	1.00	27.53	B
ATOM	3790	CB	ASN	B	186	18.311	.950	15.764	1.00	25.61	B
ATOM	3791	CG	ASN	B	186	17.664	1.811	16.824	1.00	23.84	B
ATOM	3792	OD1	ASN	B	186	16.455	2.001	16.829	1.00	22.51	B
ATOM	3793	ND2	ASN	B	186	18.472	2.335	17.732	1.00	21.61	B
ATOM	3794	C	ASN	B	186	18.592	-1.289	14.752	1.00	29.41	B
ATOM	3795	O	ASN	B	186	19.661	-1.877	14.897	1.00	25.66	B
ATOM	3796	N	TRP	B	187	17.918	-1.269	13.608	1.00	26.93	B
ATOM	3797	CA	TRP	B	187	18.390	-1.929	12.399	1.00	28.62	B
ATOM	3798	CB	TRP	B	187	17.334	-2.927	11.907	1.00	24.10	B
ATOM	3799	CG	TRP	B	187	17.697	-3.679	10.657	1.00	27.93	B
ATOM	3800	CD2	TRP	B	187	16.863	-4.596	9.936	1.00	27.28	B
ATOM	3801	CE2	TRP	B	187	17.591	-5.031	8.808	1.00	28.62	B
ATOM	3802	CE3	TRP	B	187	15.569	-5.090	10.133	1.00	32.64	B
ATOM	3803	CD1	TRP	B	187	18.872	-3.602	9.954	1.00	31.86	B
ATOM	3804	NE1	TRP	B	187	18.812	-4.411	8.841	1.00	32.70	B
ATOM	3805	CZ2	TRP	B	187	17.069	-5.935	7.883	1.00	32.01	B
ATOM	3806	CZ3	TRP	B	187	15.048	-5.990	9.206	1.00	32.53	B
ATOM	3807	CH2	TRP	B	187	15.798	-6.400	8.097	1.00	35.84	B
ATOM	3808	C	TRP	B	187	18.636	-.831	11.350	1.00	29.44	B
ATOM	3809	O	TRP	B	187	17.687	-.246	10.816	1.00	26.83	B
ATOM	3810	N	PHE	B	188	19.910	-.539	11.088	1.00	24.87	B
ATOM	3811	CA	PHE	B	188	20.288	.480	10.108	1.00	28.26	B
ATOM	3812	CB	PHE	B	188	21.422	1.341	10.651	1.00	23.82	B
ATOM	3813	CG	PHE	B	188	21.083	2.051	11.922	1.00	26.56	B
ATOM	3814	CD1	PHE	B	188	21.749	1.745	13.100	1.00	27.96	B
ATOM	3815	CD2	PHE	B	188	20.093	3.027	11.946	1.00	26.72	B
ATOM	3816	CE1	PHE	B	188	21.437	2.398	14.287	1.00	29.64	B
ATOM	3817	CE2	PHE	B	188	19.774	3.682	13.125	1.00	30.80	B
ATOM	3818	CZ	PHE	B	188	20.450	3.366	14.301	1.00	27.36	B
ATOM	3819	C	PHE	B	188	20.753	-.224	8.849	1.00	29.36	B
ATOM	3820	O	PHE	B	188	21.675	-1.033	8.907	1.00	34.19	B
ATOM	3821	N	GLU	B	189	20.137	.085	7.710	1.00	30.01	B
ATOM	3822	CA	GLU	B	189	20.504	-.591	6.473	1.00	28.74	B
ATOM	3823	CB	GLU	B	189	19.633	-1.837	6.311	1.00	28.15	B
ATOM	3824	CG	GLU	B	189	20.042	-2.740	5.173	1.00	32.33	B
ATOM	3825	CD	GLU	B	189	19.364	-4.093	5.236	1.00	37.09	B
ATOM	3826	OE1	GLU	B	189	18.255	-4.247	4.684	1.00	41.59	B
ATOM	3827	OE2	GLU	B	189	19.942	-5.011	5.855	1.00	43.25	B
ATOM	3828	C	GLU	B	189	20.418	.253	5.194	1.00	33.10	B
ATOM	3829	O	GLU	B	189	19.435	.964	4.954	1.00	26.62	B
ATOM	3830	N	ASN	B	190	21.456	.150	4.371	1.00	33.70	B
ATOM	3831	CA	ASN	B	190	21.513	.863	3.103	1.00	31.09	B
ATOM	3832	CB	ASN	B	190	20.405	.353	2.178	1.00	33.17	B
ATOM	3833	CG	ASN	B	190	20.820	.353	.724	1.00	43.73	B
ATOM	3834	OD1	ASN	B	190	21.833	-.243	.361	1.00	45.12	B
ATOM	3835	ND2	ASN	B	190	20.037	1.020	-.124	1.00	47.62	B
ATOM	3836	C	ASN	B	190	21.381	2.365	3.310	1.00	30.75	B
ATOM	3837	O	ASN	B	190	20.438	3.003	2.830	1.00	32.64	B
ATOM	3838	N	LEU	B	191	22.340	2.920	4.037	1.00	29.86	B
ATOM	3839	CA	LEU	B	191	22.377	4.338	4.335	1.00	32.46	B
ATOM	3840	CB	LEU	B	191	22.181	4.560	5.839	1.00	31.11	B
ATOM	3841	CG	LEU	B	191	20.879	4.052	6.470	1.00	24.02	B
ATOM	3842	CD1	LEU	B	191	20.964	4.180	7.972	1.00	27.26	B
ATOM	3843	CD2	LEU	B	191	19.710	4.852	5.946	1.00	25.27	B
ATOM	3844	C	LEU	B	191	23.750	4.841	3.910	1.00	34.26	B
ATOM	3845	O	LEU	B	191	24.758	4.155	4.107	1.00	34.24	B
ATOM	3846	N	ASN	B	192	23.797	6.034	3.330	1.00	33.68	B
ATOM	3847	CA	ASN	B	192	25.071	6.577	2.884	1.00	32.36	B
ATOM	3848	CB	ASN	B	192	24.842	7.684	1.855	1.00	36.18	B
ATOM	3849	CG	ASN	B	192	26.122	8.083	1.144	1.00	32.97	B
ATOM	3850	OD1	ASN	B	192	26.584	7.395	.234	1.00	34.07	B
ATOM	3851	ND2	ASN	B	192	26.715	9.185	1.577	1.00	37.64	B
ATOM	3852	C	ASN	B	192	25.951	7.106	4.022	1.00	32.61	B

ATOM	3853	O	ASN	B	192	27.095	6.673	4.184	1.00	34.71	B
ATOM	3854	N	SER	B	193	25.431	8.042	4.808	1.00	31.42	B
ATOM	3855	CA	SER	B	193	26.207	8.600	5.909	1.00	30.69	B
ATOM	3856	CB	SER	B	193	27.096	9.735	5.404	1.00	33.08	B
ATOM	3857	OG	SER	B	193	26.302	10.806	4.918	1.00	35.89	B
ATOM	3858	C	SER	B	193	25.325	9.117	7.038	1.00	29.52	B
ATOM	3859	O	SER	B	193	24.100	9.068	6.945	1.00	31.64	B
ATOM	3860	N	ARG	B	194	25.963	9.616	8.097	1.00	28.63	B
ATOM	3861	CA	ARG	B	194	25.269	10.147	9.275	1.00	29.52	B
ATOM	3862	CB	ARG	B	194	24.279	11.248	8.885	1.00	31.04	B
ATOM	3863	CG	ARG	B	194	24.862	12.441	8.159	1.00	35.19	B
ATOM	3864	CD	ARG	B	194	23.751	13.447	7.934	1.00	39.60	B
ATOM	3865	NE	ARG	B	194	24.202	14.670	7.278	1.00	40.44	B
ATOM	3866	CZ	ARG	B	194	23.401	15.692	6.981	1.00	39.78	B
ATOM	3867	NH1	ARG	B	194	22.110	15.636	7.285	1.00	36.38	B
ATOM	3868	NH2	ARG	B	194	23.889	16.767	6.372	1.00	36.92	B
ATOM	3869	C	ARG	B	194	24.496	9.028	9.964	1.00	31.44	B
ATOM	3870	O	ARG	B	194	23.271	9.043	9.990	1.00	29.79	B
ATOM	3871	N	VAL	B	195	25.201	8.060	10.534	1.00	30.43	B
ATOM	3872	CA	VAL	B	195	24.521	6.945	11.179	1.00	26.25	B
ATOM	3873	CB	VAL	B	195	24.759	5.642	10.369	1.00	28.49	B
ATOM	3874	CG1	VAL	B	195	23.683	4.609	10.693	1.00	27.66	B
ATOM	3875	CG2	VAL	B	195	24.777	5.961	8.873	1.00	26.62	B
ATOM	3876	C	VAL	B	195	24.947	6.740	12.635	1.00	26.95	B
ATOM	3877	O	VAL	B	195	25.354	5.646	13.026	1.00	28.68	B
ATOM	3878	N	PRO	B	196	24.859	7.796	13.461	1.00	26.99	B
ATOM	3879	CD	PRO	B	196	24.815	7.591	14.920	1.00	26.66	B
ATOM	3880	CA	PRO	B	196	24.400	9.149	13.134	1.00	30.83	B
ATOM	3881	CB	PRO	B	196	23.436	9.440	14.258	1.00	34.29	B
ATOM	3882	CG	PRO	B	196	24.227	8.921	15.434	1.00	34.26	B
ATOM	3883	C	PRO	B	196	25.557	10.138	13.174	1.00	33.26	B
ATOM	3884	O	PRO	B	196	26.663	9.790	13.583	1.00	34.09	B
ATOM	3885	N	SER	B	197	25.298	11.367	12.738	1.00	31.02	B
ATOM	3886	CA	SER	B	197	26.294	12.429	12.804	1.00	32.73	B
ATOM	3887	CB	SER	B	197	26.060	13.474	11.715	1.00	33.61	B
ATOM	3888	OG	SER	B	197	26.929	14.585	11.897	1.00	38.53	B
ATOM	3889	C	SER	B	197	25.974	13.009	14.175	1.00	32.05	B
ATOM	3890	O	SER	B	197	24.844	13.442	14.423	1.00	32.36	B
ATOM	3891	N	PHE	B	198	26.961	13.016	15.062	1.00	32.83	B
ATOM	3892	CA	PHE	B	198	26.749	13.454	16.432	1.00	32.42	B
ATOM	3893	CB	PHE	B	198	26.933	12.224	17.334	1.00	33.49	B
ATOM	3894	CG	PHE	B	198	26.124	12.249	18.597	1.00	37.37	B
ATOM	3895	CD1	PHE	B	198	26.544	12.986	19.702	1.00	37.07	B
ATOM	3896	CD2	PHE	B	198	24.959	11.490	18.699	1.00	37.67	B
ATOM	3897	CE1	PHE	B	198	25.816	12.959	20.894	1.00	36.80	B
ATOM	3898	CE2	PHE	B	198	24.227	11.459	19.882	1.00	38.22	B
ATOM	3899	CZ	PHE	B	198	24.656	12.193	20.982	1.00	35.07	B
ATOM	3900	C	PHE	B	198	27.662	14.595	16.888	1.00	35.47	B
ATOM	3901	O	PHE	B	198	28.843	14.382	17.155	1.00	36.39	B
ATOM	3902	N	ARG	B	199	27.098	15.800	16.983	1.00	33.78	B
ATOM	3903	CA	ARG	B	199	27.833	16.986	17.417	1.00	35.35	B
ATOM	3904	CB	ARG	B	199	27.419	18.204	16.583	1.00	34.80	B
ATOM	3905	CG	ARG	B	199	27.871	18.216	15.130	1.00	38.30	B
ATOM	3906	CD	ARG	B	199	27.352	19.485	14.483	1.00	36.34	B
ATOM	3907	NE	ARG	B	199	28.019	19.831	13.233	1.00	40.17	B
ATOM	3908	CZ	ARG	B	199	27.440	19.761	12.041	1.00	42.40	B
ATOM	3909	NH1	ARG	B	199	26.186	19.348	11.947	1.00	39.30	B
ATOM	3910	NH2	ARG	B	199	28.103	20.129	10.949	1.00	39.43	B
ATOM	3911	C	ARG	B	199	27.526	17.294	18.886	1.00	37.60	B
ATOM	3912	O	ARG	B	199	26.356	17.421	19.261	1.00	35.69	B
ATOM	3913	N	PHE	B	200	28.565	17.432	19.706	1.00	35.25	B
ATOM	3914	CA	PHE	B	200	28.398	17.740	21.133	1.00	35.74	B
ATOM	3915	CB	PHE	B	200	27.668	19.085	21.342	1.00	38.33	B
ATOM	3916	CG	PHE	B	200	28.285	20.259	20.615	1.00	39.24	B
ATOM	3917	CD1	PHE	B	200	27.886	20.580	19.321	1.00	36.86	B
ATOM	3918	CD2	PHE	B	200	29.237	21.065	21.244	1.00	39.40	B
ATOM	3919	CE1	PHE	B	200	28.423	21.697	18.654	1.00	40.58	B
ATOM	3920	CE2	PHE	B	200	29.781	22.183	20.591	1.00	38.87	B
ATOM	3921	CZ	PHE	B	200	29.372	22.501	19.293	1.00	38.57	B

ATOM	3922	C	PHE	B	200	27.586	16.658	21.843	1.00	37.98	B
ATOM	3923	O	PHE	B	200	27.204	15.661	21.233	1.00	39.14	B
ATOM	3924	N	GLY	B	201	27.337	16.868	23.137	1.00	38.52	B
ATOM	3925	CA	GLY	B	201	26.537	15.946	23.926	1.00	35.30	B
ATOM	3926	C	GLY	B	201	27.108	14.599	24.348	1.00	38.40	B
ATOM	3927	O	GLY	B	201	28.308	14.314	24.209	1.00	37.96	B
ATOM	3928	N	GLU	B	202	26.211	13.761	24.863	1.00	33.97	B
ATOM	3929	CA	GLU	B	202	26.540	12.421	25.338	1.00	32.07	B
ATOM	3930	CB	GLU	B	202	26.275	12.306	26.843	1.00	34.16	B
ATOM	3931	CG	GLU	B	202	27.104	13.212	27.712	1.00	35.06	B
ATOM	3932	CD	GLU	B	202	26.565	13.303	29.121	1.00	35.16	B
ATOM	3933	OE1	GLU	B	202	26.181	12.260	29.682	1.00	44.00	B
ATOM	3934	OE2	GLU	B	202	26.533	14.410	29.679	1.00	43.59	B
ATOM	3935	C	GLU	B	202	25.657	11.413	24.624	1.00	32.85	B
ATOM	3936	O	GLU	B	202	24.437	11.592	24.532	1.00	31.76	B
ATOM	3937	N	GLY	B	203	26.268	10.343	24.133	1.00	28.26	B
ATOM	3938	CA	GLY	B	203	25.500	9.330	23.448	1.00	27.15	B
ATOM	3939	C	GLY	B	203	25.836	7.921	23.902	1.00	31.66	B
ATOM	3940	O	GLY	B	203	26.863	7.677	24.550	1.00	34.25	B
ATOM	3941	N	HIS	B	204	24.953	6.991	23.564	1.00	28.75	B
ATOM	3942	CA	HIS	B	204	25.142	5.585	23.890	1.00	30.34	B
ATOM	3943	CB	HIS	B	204	24.405	5.216	25.181	1.00	28.82	B
ATOM	3944	CG	HIS	B	204	24.769	3.868	25.721	1.00	32.32	B
ATOM	3945	CD2	HIS	B	204	25.714	2.975	25.336	1.00	35.20	B
ATOM	3946	ND1	HIS	B	204	24.117	3.297	26.791	1.00	30.53	B
ATOM	3947	CE1	HIS	B	204	24.639	2.108	27.039	1.00	35.44	B
ATOM	3948	NE2	HIS	B	204	25.611	1.889	26.171	1.00	36.89	B
ATOM	3949	C	HIS	B	204	24.564	4.805	22.720	1.00	31.51	B
ATOM	3950	O	HIS	B	204	23.367	4.878	22.441	1.00	28.72	B
ATOM	3951	N	ILE	B	205	25.420	4.065	22.030	1.00	30.11	B
ATOM	3952	CA	ILE	B	205	24.993	3.282	20.885	1.00	26.19	B
ATOM	3953	CB	ILE	B	205	25.704	3.786	19.601	1.00	27.51	B
ATOM	3954	CG2	ILE	B	205	25.216	3.013	18.392	1.00	23.80	B
ATOM	3955	CG1	ILE	B	205	25.451	5.286	19.433	1.00	25.55	B
ATOM	3956	CD1	ILE	B	205	26.150	5.924	18.237	1.00	29.73	B
ATOM	3957	C	ILE	B	205	25.343	1.823	21.143	1.00	30.59	B
ATOM	3958	O	ILE	B	205	26.515	1.448	21.133	1.00	32.68	B
ATOM	3959	N	TYR	B	206	24.332	.992	21.378	1.00	30.13	B
ATOM	3960	CA	TYR	B	206	24.592	-.416	21.659	1.00	28.43	B
ATOM	3961	CB	TYR	B	206	24.744	-.625	23.174	1.00	28.24	B
ATOM	3962	CG	TYR	B	206	23.461	-.532	23.980	1.00	25.76	B
ATOM	3963	CD1	TYR	B	206	22.675	-1.659	24.211	1.00	31.29	B
ATOM	3964	CE1	TYR	B	206	21.522	-1.586	24.993	1.00	32.92	B
ATOM	3965	CD2	TYR	B	206	23.058	.674	24.544	1.00	27.60	B
ATOM	3966	CE2	TYR	B	206	21.910	.757	25.328	1.00	31.22	B
ATOM	3967	CZ	TYR	B	206	21.150	-.373	25.550	1.00	29.75	B
ATOM	3968	OH	TYR	B	206	20.024	-.294	26.335	1.00	36.59	B
ATOM	3969	C	TYR	B	206	23.560	-1.392	21.104	1.00	31.00	B
ATOM	3970	O	TYR	B	206	22.390	-1.045	20.882	1.00	28.97	B
ATOM	3971	N	ASN	B	207	24.018	-2.620	20.883	1.00	27.99	B
ATOM	3972	CA	ASN	B	207	23.187	-3.690	20.364	1.00	27.98	B
ATOM	3973	CB	ASN	B	207	22.215	-4.184	21.451	1.00	28.55	B
ATOM	3974	CG	ASN	B	207	22.903	-5.037	22.530	1.00	37.96	B
ATOM	3975	OD1	ASN	B	207	22.372	-5.206	23.634	1.00	33.92	B
ATOM	3976	ND2	ASN	B	207	24.080	-5.583	22.209	1.00	32.30	B
ATOM	3977	C	ASN	B	207	22.415	-3.294	19.111	1.00	28.97	B
ATOM	3978	O	ASN	B	207	21.257	-3.674	18.948	1.00	29.05	B
ATOM	3979	N	ASN	B	208	23.048	-2.525	18.230	1.00	27.99	B
ATOM	3980	CA	ASN	B	208	22.417	-2.127	16.969	1.00	28.63	B
ATOM	3981	CB	ASN	B	208	22.685	-.656	16.641	1.00	27.46	B
ATOM	3982	CG	ASN	B	208	22.117	.291	17.675	1.00	27.77	B
ATOM	3983	OD1	ASN	B	208	20.907	.496	17.743	1.00	32.69	B
ATOM	3984	ND2	ASN	B	208	22.994	.876	18.492	1.00	26.46	B
ATOM	3985	C	ASN	B	208	23.032	-2.967	15.859	1.00	29.00	B
ATOM	3986	O	ASN	B	208	24.155	-3.445	15.982	1.00	26.87	B
ATOM	3987	N	TYR	B	209	22.295	-3.130	14.771	1.00	28.51	B
ATOM	3988	CA	TYR	B	209	22.781	-3.881	13.628	1.00	31.58	B
ATOM	3989	CB	TYR	B	209	21.805	-5.010	13.294	1.00	29.18	B
ATOM	3990	CG	TYR	B	209	22.091	-5.710	11.990	1.00	32.82	B

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ATOM   3991  CD1 TYR B 209      23.386  -6.130  11.668  1.00 32.46      B
ATOM   3992  CE1 TYR B 209      23.652  -6.781  10.460  1.00 36.05      B
ATOM   3993  CD2 TYR B 209      21.066  -5.961  11.072  1.00 32.57      B
ATOM   3994  CE2 TYR B 209      21.323  -6.614   9.860  1.00 30.86      B
ATOM   3995  CZ  TYR B 209      22.615  -7.020   9.564  1.00 35.51      B
ATOM   3996  OH  TYR B 209      22.871  -7.681   8.382  1.00 36.24      B
ATOM   3997  C   TYR B 209      22.924  -2.928  12.437  1.00 32.77      B
ATOM   3998  O   TYR B 209      21.934  -2.364  11.976  1.00 31.28      B
ATOM   3999  N   PHE B 210      24.156  -2.730  11.968  1.00 32.24      B
ATOM   4000  CA  PHE B 210      24.419  -1.854  10.821  1.00 32.91      B
ATOM   4001  CB  PHE B 210      25.606   -.929  11.074  1.00 31.15      B
ATOM   4002  CG  PHE B 210      25.440    .000  12.235  1.00 31.75      B
ATOM   4003  CD1 PHE B 210      25.539   -.466  13.543  1.00 33.96      B
ATOM   4004  CD2 PHE B 210      25.254   1.363  12.020  1.00 31.93      B
ATOM   4005  CE1 PHE B 210      25.463    .415  14.622  1.00 30.33      B
ATOM   4006  CE2 PHE B 210      25.174   2.252  13.088  1.00 31.45      B
ATOM   4007  CZ  PHE B 210      25.281   1.778  14.392  1.00 32.21      B
ATOM   4008  C   PHE B 210      24.773  -2.703   9.606  1.00 36.48      B
ATOM   4009  O   PHE B 210      25.686  -3.524   9.676  1.00 41.31      B
ATOM   4010  N   ASN B 211      24.072  -2.506   8.494  1.00 33.78      B
ATOM   4011  CA  ASN B 211      24.366  -3.263   7.280  1.00 35.45      B
ATOM   4012  CB  ASN B 211      23.369  -4.415   7.116  1.00 30.94      B
ATOM   4013  CG  ASN B 211      23.649  -5.262   5.889  1.00 30.54      B
ATOM   4014  OD1 ASN B 211      24.786  -5.654   5.635  1.00 35.31      B
ATOM   4015  ND2 ASN B 211      22.606  -5.559   5.130  1.00 33.49      B
ATOM   4016  C   ASN B 211      24.328  -2.349   6.047  1.00 38.08      B
ATOM   4017  O   ASN B 211      23.380  -1.582   5.856  1.00 37.31      B
ATOM   4018  N   LYS B 212      25.362  -2.445   5.210  1.00 38.80      B
ATOM   4019  CA  LYS B 212      25.475  -1.625   4.005  1.00 37.28      B
ATOM   4020  CB  LYS B 212      24.300  -1.856   3.066  1.00 36.80      B
ATOM   4021  CG  LYS B 212      24.206  -3.251   2.503  1.00 41.13      B
ATOM   4022  CD  LYS B 212      23.073  -3.308   1.506  1.00 46.98      B
ATOM   4023  CE  LYS B 212      22.837  -4.699    .979  1.00 52.12      B
ATOM   4024  NZ  LYS B 212      21.679  -4.684    .030  1.00 58.19      B
ATOM   4025  C   LYS B 212      25.569   -.135   4.288  1.00 35.10      B
ATOM   4026  O   LYS B 212      24.703    .636   3.874  1.00 35.96      B
ATOM   4027  N   ILE B 213      26.602    .271   5.012  1.00 33.79      B
ATOM   4028  CA  ILE B 213      26.807   1.684   5.290  1.00 33.50      B
ATOM   4029  CB  ILE B 213      27.471   1.894   6.655  1.00 34.25      B
ATOM   4030  CG2 ILE B 213      27.538   3.371   6.974  1.00 32.77      B
ATOM   4031  CG1 ILE B 213      26.675   1.148   7.740  1.00 35.96      B
ATOM   4032  CD1 ILE B 213      25.200   1.508   7.807  1.00 32.79      B
ATOM   4033  C   ILE B 213      27.746   2.094   4.159  1.00 38.10      B
ATOM   4034  O   ILE B 213      28.925   1.729   4.147  1.00 38.99      B
ATOM   4035  N   ILE B 214      27.203   2.845   3.205  1.00 39.06      B
ATOM   4036  CA  ILE B 214      27.930   3.247   2.005  1.00 39.36      B
ATOM   4037  CB  ILE B 214      26.977   3.919    .982  1.00 39.82      B
ATOM   4038  CG2 ILE B 214      27.601   3.888   -.410  1.00 43.03      B
ATOM   4039  CG1 ILE B 214      25.633   3.176    .940  1.00 40.17      B
ATOM   4040  CD1 ILE B 214      25.749   1.672    .785  1.00 40.31      B
ATOM   4041  C   ILE B 214      29.161   4.121   2.143  1.00 40.48      B
ATOM   4042  O   ILE B 214      30.229   3.754   1.663  1.00 43.99      B
ATOM   4043  N   ASP B 215      29.041   5.272   2.793  1.00 40.75      B
ATOM   4044  CA  ASP B 215      30.202   6.141   2.904  1.00 39.03      B
ATOM   4045  CB  ASP B 215      29.850   7.540   2.396  1.00 41.50      B
ATOM   4046  CG  ASP B 215      31.080   8.361   2.088  1.00 45.26      B
ATOM   4047  OD1 ASP B 215      31.999   7.813   1.436  1.00 50.15      B
ATOM   4048  OD2 ASP B 215      31.132   9.545   2.484  1.00 45.05      B
ATOM   4049  C   ASP B 215      30.813   6.222   4.294  1.00 42.28      B
ATOM   4050  O   ASP B 215      32.040   6.179   4.446  1.00 42.20      B
ATOM   4051  N   SER B 216      29.968   6.352   5.312  1.00 39.36      B
ATOM   4052  CA  SER B 216      30.447   6.420   6.684  1.00 34.45      B
ATOM   4053  CB  SER B 216      31.179   7.745   6.937  1.00 35.92      B
ATOM   4054  OG  SER B 216      30.323   8.853   6.754  1.00 35.42      B
ATOM   4055  C   SER B 216      29.272   6.259   7.646  1.00 36.18      B
ATOM   4056  O   SER B 216      28.135   6.623   7.328  1.00 30.77      B
ATOM   4057  N   GLY B 217      29.556   5.705   8.820  1.00 36.75      B
ATOM   4058  CA  GLY B 217      28.510   5.476   9.795  1.00 35.09      B
ATOM   4059  C   GLY B 217      28.464   6.473  10.931  1.00 35.43      B
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ATOM	4060	O	GLY	B	217	28.033	7.611	10.755	1.00	38.53	B
ATOM	4061	N	ILE	B	218	28.901	6.038	12.106	1.00	34.18	B
ATOM	4062	CA	ILE	B	218	28.891	6.891	13.285	1.00	30.69	B
ATOM	4063	CB	ILE	B	218	29.152	6.065	14.558	1.00	28.86	B
ATOM	4064	CG2	ILE	B	218	29.047	6.948	15.778	1.00	30.24	B
ATOM	4065	CG1	ILE	B	218	28.158	4.909	14.642	1.00	29.60	B
ATOM	4066	CD1	ILE	B	218	28.467	3.924	15.756	1.00	32.56	B
ATOM	4067	C	ILE	B	218	29.960	7.965	13.181	1.00	35.90	B
ATOM	4068	O	ILE	B	218	31.153	7.658	13.085	1.00	37.46	B
ATOM	4069	N	ASN	B	219	29.538	9.223	13.200	1.00	34.19	B
ATOM	4070	CA	ASN	B	219	30.481	10.327	13.122	1.00	33.70	B
ATOM	4071	CB	ASN	B	219	30.188	11.196	11.890	1.00	38.20	B
ATOM	4072	CG	ASN	B	219	31.224	12.296	11.689	1.00	38.89	B
ATOM	4073	OD1	ASN	B	219	32.256	12.325	12.365	1.00	38.00	B
ATOM	4074	ND2	ASN	B	219	30.957	13.200	10.750	1.00	35.49	B
ATOM	4075	C	ASN	B	219	30.390	11.164	14.390	1.00	34.62	B
ATOM	4076	O	ASN	B	219	29.483	11.982	14.545	1.00	36.48	B
ATOM	4077	N	SER	B	220	31.327	10.934	15.301	1.00	34.21	B
ATOM	4078	CA	SER	B	220	31.361	11.660	16.554	1.00	34.57	B
ATOM	4079	CB	SER	B	220	32.068	10.831	17.627	1.00	33.37	B
ATOM	4080	OG	SER	B	220	32.057	11.505	18.869	1.00	35.89	B
ATOM	4081	C	SER	B	220	32.113	12.951	16.325	1.00	37.24	B
ATOM	4082	O	SER	B	220	33.212	12.937	15.765	1.00	41.29	B
ATOM	4083	N	ARG	B	221	31.533	14.068	16.754	1.00	37.21	B
ATOM	4084	CA	ARG	B	221	32.193	15.344	16.570	1.00	36.89	B
ATOM	4085	CB	ARG	B	221	31.935	15.860	15.168	1.00	40.58	B
ATOM	4086	CG	ARG	B	221	30.556	15.654	14.588	1.00	40.70	B
ATOM	4087	CD	ARG	B	221	30.831	16.024	13.173	1.00	40.65	B
ATOM	4088	NE	ARG	B	221	29.803	15.959	12.213	1.00	43.00	B
ATOM	4089	CZ	ARG	B	221	29.531	16.763	11.193	1.00	42.04	B
ATOM	4090	NH1	ARG	B	221	30.195	17.873	10.875	1.00	42.14	B
ATOM	4091	NH2	ARG	B	221	28.564	16.333	10.409	1.00	41.04	B
ATOM	4092	C	ARG	B	221	31.905	16.447	17.563	1.00	39.89	B
ATOM	4093	O	ARG	B	221	30.998	16.354	18.392	1.00	41.52	B
ATOM	4094	N	MET	B	222	32.709	17.499	17.467	1.00	39.30	B
ATOM	4095	CA	MET	B	222	32.604	18.659	18.340	1.00	38.12	B
ATOM	4096	CB	MET	B	222	31.388	19.506	17.957	1.00	38.66	B
ATOM	4097	CG	MET	B	222	31.499	20.147	16.570	1.00	43.79	B
ATOM	4098	SD	MET	B	222	32.953	21.262	16.403	1.00	50.29	B
ATOM	4099	CE	MET	B	222	32.408	22.641	17.363	1.00	39.01	B
ATOM	4100	C	MET	B	222	32.570	18.307	19.827	1.00	39.38	B
ATOM	4101	O	MET	B	222	31.720	18.790	20.578	1.00	40.80	B
ATOM	4102	N	GLY	B	223	33.508	17.460	20.245	1.00	39.84	B
ATOM	4103	CA	GLY	B	223	33.609	17.089	21.647	1.00	40.20	B
ATOM	4104	C	GLY	B	223	32.586	16.107	22.174	1.00	41.00	B
ATOM	4105	O	GLY	B	223	32.463	15.934	23.387	1.00	39.73	B
ATOM	4106	N	ALA	B	224	31.852	15.464	21.276	1.00	37.23	B
ATOM	4107	CA	ALA	B	224	30.850	14.507	21.694	1.00	38.50	B
ATOM	4108	CB	ALA	B	224	30.040	14.035	20.486	1.00	33.26	B
ATOM	4109	C	ALA	B	224	31.521	13.316	22.365	1.00	41.57	B
ATOM	4110	O	ALA	B	224	32.636	12.926	22.015	1.00	42.34	B
ATOM	4111	N	ARG	B	225	30.841	12.743	23.344	1.00	39.68	B
ATOM	4112	CA	ARG	B	225	31.363	11.576	24.017	1.00	40.77	B
ATOM	4113	CB	ARG	B	225	31.566	11.855	25.497	1.00	46.54	B
ATOM	4114	CG	ARG	B	225	32.841	12.634	25.777	1.00	57.21	B
ATOM	4115	CD	ARG	B	225	33.030	12.766	27.259	1.00	63.18	B
ATOM	4116	NE	ARG	B	225	31.912	13.494	27.844	1.00	69.42	B
ATOM	4117	CZ	ARG	B	225	31.455	13.283	29.074	1.00	72.70	B
ATOM	4118	NH1	ARG	B	225	30.430	13.998	29.532	1.00	73.86	B
ATOM	4119	NH2	ARG	B	225	32.017	12.347	29.837	1.00	72.11	B
ATOM	4120	C	ARG	B	225	30.326	10.500	23.806	1.00	38.37	B
ATOM	4121	O	ARG	B	225	29.188	10.616	24.262	1.00	36.28	B
ATOM	4122	N	ILE	B	226	30.723	9.451	23.106	1.00	34.97	B
ATOM	4123	CA	ILE	B	226	29.802	8.377	22.812	1.00	30.53	B
ATOM	4124	CB	ILE	B	226	29.478	8.341	21.311	1.00	31.73	B
ATOM	4125	CG2	ILE	B	226	28.343	7.357	21.048	1.00	23.31	B
ATOM	4126	CG1	ILE	B	226	29.098	9.742	20.826	1.00	31.40	B
ATOM	4127	CD1	ILE	B	226	28.785	9.807	19.353	1.00	30.60	B
ATOM	4128	C	ILE	B	226	30.316	7.005	23.200	1.00	35.97	B

ATOM	4129	O	ILE	B	226	31.424	6.610	22.820	1.00	36.12	B
ATOM	4130	N	ARG	B	227	29.498	6.282	23.959	1.00	33.28	B
ATOM	4131	CA	ARG	B	227	29.824	4.929	24.373	1.00	33.51	B
ATOM	4132	CB	ARG	B	227	29.143	4.620	25.706	1.00	30.74	B
ATOM	4133	CG	ARG	B	227	29.314	3.207	26.202	1.00	35.11	B
ATOM	4134	CD	ARG	B	227	30.740	2.941	26.635	1.00	40.25	B
ATOM	4135	NE	ARG	B	227	30.806	1.662	27.321	1.00	43.85	B
ATOM	4136	CZ	ARG	B	227	30.983	1.516	28.631	1.00	43.47	B
ATOM	4137	NH1	ARG	B	227	31.126	2.572	29.417	1.00	44.06	B
ATOM	4138	NH2	ARG	B	227	30.991	.301	29.156	1.00	44.57	B
ATOM	4139	C	ARG	B	227	29.247	4.060	23.258	1.00	32.38	B
ATOM	4140	O	ARG	B	227	28.043	4.078	23.024	1.00	35.20	B
ATOM	4141	N	ILE	B	228	30.104	3.316	22.564	1.00	32.46	B
ATOM	4142	CA	ILE	B	228	29.675	2.462	21.461	1.00	28.84	B
ATOM	4143	CB	ILE	B	228	30.346	2.918	20.150	1.00	29.51	B
ATOM	4144	CG2	ILE	B	228	29.768	2.155	18.974	1.00	29.86	B
ATOM	4145	CG1	ILE	B	228	30.165	4.434	19.985	1.00	28.36	B
ATOM	4146	CD1	ILE	B	228	31.035	5.060	18.913	1.00	29.40	B
ATOM	4147	C	ILE	B	228	30.087	1.027	21.764	1.00	33.28	B
ATOM	4148	O	ILE	B	228	31.277	.701	21.724	1.00	36.70	B
ATOM	4149	N	GLU	B	229	29.117	.159	22.038	1.00	33.66	B
ATOM	4150	CA	GLU	B	229	29.454	-1.216	22.383	1.00	35.57	B
ATOM	4151	CB	GLU	B	229	29.602	-1.317	23.908	1.00	35.51	B
ATOM	4152	CG	GLU	B	229	28.282	-1.199	24.669	1.00	36.60	B
ATOM	4153	CD	GLU	B	229	28.441	-.643	26.086	1.00	40.40	B
ATOM	4154	OE1	GLU	B	229	29.505	-.853	26.709	1.00	39.11	B
ATOM	4155	OE2	GLU	B	229	27.487	-.005	26.592	1.00	37.75	B
ATOM	4156	C	GLU	B	229	28.479	-2.283	21.888	1.00	36.31	B
ATOM	4157	O	GLU	B	229	27.299	-2.013	21.660	1.00	37.58	B
ATOM	4158	N	ASN	B	230	28.994	-3.498	21.714	1.00	34.32	B
ATOM	4159	CA	ASN	B	230	28.199	-4.640	21.278	1.00	31.71	B
ATOM	4160	CB	ASN	B	230	27.349	-5.149	22.447	1.00	33.82	B
ATOM	4161	CG	ASN	B	230	28.183	-5.752	23.574	1.00	38.47	B
ATOM	4162	OD1	ASN	B	230	29.205	-5.197	23.987	1.00	38.06	B
ATOM	4163	ND2	ASN	B	230	27.732	-6.891	24.089	1.00	38.43	B
ATOM	4164	C	ASN	B	230	27.304	-4.379	20.065	1.00	34.00	B
ATOM	4165	O	ASN	B	230	26.131	-4.777	20.046	1.00	32.98	B
ATOM	4166	N	ASN	B	231	27.858	-3.712	19.056	1.00	32.27	B
ATOM	4167	CA	ASN	B	231	27.136	-3.434	17.823	1.00	31.08	B
ATOM	4168	CB	ASN	B	231	27.355	-1.987	17.371	1.00	31.03	B
ATOM	4169	CG	ASN	B	231	26.737	-.981	18.303	1.00	26.80	B
ATOM	4170	OD1	ASN	B	231	25.518	-.812	18.332	1.00	26.08	B
ATOM	4171	ND2	ASN	B	231	27.576	-.302	19.076	1.00	26.29	B
ATOM	4172	C	ASN	B	231	27.717	-4.343	16.755	1.00	33.70	B
ATOM	4173	O	ASN	B	231	28.875	-4.735	16.843	1.00	37.22	B
ATOM	4174	N	LEU	B	232	26.921	-4.686	15.752	1.00	32.41	B
ATOM	4175	CA	LEU	B	232	27.423	-5.502	14.656	1.00	32.86	B
ATOM	4176	CB	LEU	B	232	26.570	-6.756	14.447	1.00	33.96	B
ATOM	4177	CG	LEU	B	232	26.923	-7.478	13.138	1.00	36.70	B
ATOM	4178	CD1	LEU	B	232	28.338	-8.029	13.219	1.00	40.39	B
ATOM	4179	CD2	LEU	B	232	25.931	-8.590	12.870	1.00	40.11	B
ATOM	4180	C	LEU	B	232	27.397	-4.670	13.377	1.00	33.96	B
ATOM	4181	O	LEU	B	232	26.350	-4.131	13.003	1.00	35.91	B
ATOM	4182	N	PHE	B	233	28.546	-4.555	12.717	1.00	34.51	B
ATOM	4183	CA	PHE	B	233	28.634	-3.800	11.462	1.00	35.36	B
ATOM	4184	CB	PHE	B	233	29.756	-2.757	11.502	1.00	33.30	B
ATOM	4185	CG	PHE	B	233	29.637	-1.749	12.605	1.00	34.10	B
ATOM	4186	CD1	PHE	B	233	30.112	-2.032	13.877	1.00	32.75	B
ATOM	4187	CD2	PHE	B	233	29.086	-.493	12.360	1.00	36.94	B
ATOM	4188	CE1	PHE	B	233	30.048	-1.080	14.891	1.00	34.74	B
ATOM	4189	CE2	PHE	B	233	29.015	.466	13.365	1.00	32.10	B
ATOM	4190	CZ	PHE	B	233	29.498	.174	14.633	1.00	33.44	B
ATOM	4191	C	PHE	B	233	28.939	-4.759	10.311	1.00	36.55	B
ATOM	4192	O	PHE	B	233	29.956	-5.447	10.335	1.00	38.53	B
ATOM	4193	N	GLU	B	234	28.059	-4.816	9.315	1.00	37.91	B
ATOM	4194	CA	GLU	B	234	28.270	-5.670	8.146	1.00	38.57	B
ATOM	4195	CB	GLU	B	234	27.152	-6.703	7.992	1.00	38.41	B
ATOM	4196	CG	GLU	B	234	27.308	-7.928	8.859	1.00	48.58	B
ATOM	4197	CD	GLU	B	234	26.206	-8.943	8.636	1.00	48.36	B

ATOM	4198	OE1	GLU	B	234	26.264	-10.020	9.259	1.00	55.52	B
ATOM	4199	OE2	GLU	B	234	25.280	-8.671	7.841	1.00	52.74	B
ATOM	4200	C	GLU	B	234	28.290	-4.805	6.901	1.00	38.56	B
ATOM	4201	O	GLU	B	234	27.463	-3.901	6.760	1.00	38.35	B
ATOM	4202	N	ASN	B	235	29.224	-5.093	5.995	1.00	38.65	B
ATOM	4203	CA	ASN	B	235	29.351	-4.346	4.744	1.00	35.66	B
ATOM	4204	CB	ASN	B	235	28.202	-4.710	3.797	1.00	39.28	B
ATOM	4205	CG	ASN	B	235	28.047	-6.210	3.619	1.00	49.24	B
ATOM	4206	OD1	ASN	B	235	29.024	-6.909	3.337	1.00	52.50	B
ATOM	4207	ND2	ASN	B	235	26.820	-6.715	3.777	1.00	52.09	B
ATOM	4208	C	ASN	B	235	29.316	-2.855	5.043	1.00	34.30	B
ATOM	4209	O	ASN	B	235	28.477	-2.132	4.519	1.00	32.86	B
ATOM	4210	N	ALA	B	236	30.230	-2.403	5.892	1.00	35.31	B
ATOM	4211	CA	ALA	B	236	30.285	-.999	6.275	1.00	37.71	B
ATOM	4212	CB	ALA	B	236	29.982	-.855	7.754	1.00	36.48	B
ATOM	4213	C	ALA	B	236	31.627	-.361	5.973	1.00	40.92	B
ATOM	4214	O	ALA	B	236	32.681	-.966	6.192	1.00	43.12	B
ATOM	4215	N	LYS	B	237	31.579	.866	5.468	1.00	38.18	B
ATOM	4216	CA	LYS	B	237	32.782	1.613	5.158	1.00	39.22	B
ATOM	4217	CB	LYS	B	237	32.691	2.214	3.758	1.00	41.83	B
ATOM	4218	CG	LYS	B	237	33.805	3.202	3.440	1.00	40.49	B
ATOM	4219	CD	LYS	B	237	33.634	3.807	2.063	1.00	39.68	B
ATOM	4220	CE	LYS	B	237	34.597	4.964	1.877	1.00	40.05	B
ATOM	4221	NZ	LYS	B	237	34.389	6.005	2.913	1.00	38.95	B
ATOM	4222	C	LYS	B	237	32.877	2.724	6.190	1.00	42.78	B
ATOM	4223	O	LYS	B	237	31.921	3.478	6.384	1.00	45.57	B
ATOM	4224	N	ASP	B	238	34.018	2.816	6.864	1.00	40.68	B
ATOM	4225	CA	ASP	B	238	34.222	3.842	7.877	1.00	41.80	B
ATOM	4226	CB	ASP	B	238	34.425	5.195	7.190	1.00	41.31	B
ATOM	4227	CG	ASP	B	238	35.711	5.237	6.365	1.00	44.11	B
ATOM	4228	OD1	ASP	B	238	36.795	5.073	6.964	1.00	39.60	B
ATOM	4229	OD2	ASP	B	238	35.640	5.421	5.126	1.00	44.74	B
ATOM	4230	C	ASP	B	238	33.053	3.890	8.865	1.00	42.33	B
ATOM	4231	O	ASP	B	238	32.383	4.916	9.018	1.00	41.92	B
ATOM	4232	N	PRO	B	239	32.808	2.772	9.571	1.00	42.52	B
ATOM	4233	CD	PRO	B	239	33.530	1.491	9.475	1.00	40.83	B
ATOM	4234	CA	PRO	B	239	31.713	2.687	10.548	1.00	37.76	B
ATOM	4235	CB	PRO	B	239	31.709	1.209	10.938	1.00	37.22	B
ATOM	4236	CG	PRO	B	239	33.142	.809	10.770	1.00	44.37	B
ATOM	4237	C	PRO	B	239	31.823	3.624	11.746	1.00	37.43	B
ATOM	4238	O	PRO	B	239	30.811	3.990	12.342	1.00	40.22	B
ATOM	4239	N	ILE	B	240	33.040	4.017	12.105	1.00	36.22	B
ATOM	4240	CA	ILE	B	240	33.237	4.931	13.226	1.00	34.25	B
ATOM	4241	CB	ILE	B	240	33.653	4.178	14.505	1.00	31.58	B
ATOM	4242	CG2	ILE	B	240	33.838	5.155	15.653	1.00	29.63	B
ATOM	4243	CG1	ILE	B	240	32.588	3.146	14.869	1.00	32.90	B
ATOM	4244	CD1	ILE	B	240	32.970	2.274	16.055	1.00	35.67	B
ATOM	4245	C	ILE	B	240	34.323	5.950	12.884	1.00	38.78	B
ATOM	4246	O	ILE	B	240	35.491	5.591	12.711	1.00	43.53	B
ATOM	4247	N	VAL	B	241	33.943	7.220	12.792	1.00	37.00	B
ATOM	4248	CA	VAL	B	241	34.896	8.274	12.463	1.00	36.64	B
ATOM	4249	CB	VAL	B	241	34.870	8.624	10.948	1.00	35.76	B
ATOM	4250	CG1	VAL	B	241	35.235	7.408	10.107	1.00	35.20	B
ATOM	4251	CG2	VAL	B	241	33.492	9.135	10.561	1.00	37.72	B
ATOM	4252	C	VAL	B	241	34.606	9.564	13.221	1.00	40.82	B
ATOM	4253	O	VAL	B	241	33.660	9.648	14.011	1.00	41.98	B
ATOM	4254	N	SER	B	242	35.453	10.559	12.982	1.00	39.67	B
ATOM	4255	CA	SER	B	242	35.302	11.885	13.562	1.00	43.35	B
ATOM	4256	CB	SER	B	242	36.241	12.086	14.753	1.00	38.88	B
ATOM	4257	OG	SER	B	242	36.014	13.361	15.339	1.00	43.26	B
ATOM	4258	C	SER	B	242	35.700	12.808	12.418	1.00	45.17	B
ATOM	4259	O	SER	B	242	36.837	13.285	12.353	1.00	49.25	B
ATOM	4260	N	TRP	B	243	34.764	13.039	11.501	1.00	46.17	B
ATOM	4261	CA	TRP	B	243	35.032	13.874	10.327	1.00	44.62	B
ATOM	4262	CB	TRP	B	243	34.810	13.098	9.025	1.00	41.31	B
ATOM	4263	CG	TRP	B	243	35.646	11.892	8.781	1.00	43.31	B
ATOM	4264	CD2	TRP	B	243	35.400	10.890	7.792	1.00	39.99	B
ATOM	4265	CE2	TRP	B	243	36.468	9.968	7.854	1.00	37.74	B
ATOM	4266	CE3	TRP	B	243	34.376	10.684	6.854	1.00	41.38	B

ATOM	4267	CD1	TRP	B	243	36.821	11.549	9.394	1.00	43.75	B
ATOM	4268	NE1	TRP	B	243	37.321	10.392	8.840	1.00	43.35	B
ATOM	4269	CZ2	TRP	B	243	36.546	8.853	7.013	1.00	40.78	B
ATOM	4270	CZ3	TRP	B	243	34.453	9.572	6.012	1.00	40.25	B
ATOM	4271	CH2	TRP	B	243	35.533	8.671	6.100	1.00	41.94	B
ATOM	4272	C	TRP	B	243	34.169	15.111	10.193	1.00	43.86	B
ATOM	4273	O	TRP	B	243	33.140	15.252	10.850	1.00	46.76	B
ATOM	4274	N	TYR	B	244	34.613	15.994	9.303	1.00	44.34	B
ATOM	4275	CA	TYR	B	244	33.892	17.212	8.942	1.00	44.57	B
ATOM	4276	CB	TYR	B	244	32.514	16.819	8.415	1.00	42.89	B
ATOM	4277	CG	TYR	B	244	32.551	15.709	7.391	1.00	44.37	B
ATOM	4278	CD1	TYR	B	244	31.663	14.631	7.467	1.00	43.54	B
ATOM	4279	CE1	TYR	B	244	31.673	13.617	6.512	1.00	46.78	B
ATOM	4280	CD2	TYR	B	244	33.455	15.746	6.332	1.00	46.26	B
ATOM	4281	CE2	TYR	B	244	33.475	14.732	5.366	1.00	46.89	B
ATOM	4282	CZ	TYR	B	244	32.579	13.674	5.464	1.00	47.64	B
ATOM	4283	OH	TYR	B	244	32.583	12.676	4.510	1.00	50.27	B
ATOM	4284	C	TYR	B	244	33.716	18.353	9.933	1.00	46.86	B
ATOM	4285	O	TYR	B	244	33.031	19.324	9.609	1.00	50.18	B
ATOM	4286	N	SER	B	245	34.296	18.267	11.126	1.00	45.08	B
ATOM	4287	CA	SER	B	245	34.143	19.366	12.082	1.00	47.53	B
ATOM	4288	CB	SER	B	245	33.307	18.925	13.295	1.00	46.59	B
ATOM	4289	OG	SER	B	245	31.947	18.712	12.928	1.00	43.91	B
ATOM	4290	C	SER	B	245	35.492	19.911	12.549	1.00	49.04	B
ATOM	4291	O	SER	B	245	36.517	19.222	12.474	1.00	51.58	B
ATOM	4292	N	SER	B	246	35.478	21.158	13.018	1.00	47.32	B
ATOM	4293	CA	SER	B	246	36.678	21.835	13.504	1.00	48.47	B
ATOM	4294	CB	SER	B	246	36.343	23.290	13.806	1.00	48.52	B
ATOM	4295	OG	SER	B	246	35.198	23.347	14.648	1.00	49.62	B
ATOM	4296	C	SER	B	246	37.270	21.178	14.750	1.00	50.56	B
ATOM	4297	O	SER	B	246	38.491	21.232	14.978	1.00	53.16	B
ATOM	4298	N	SER	B	247	36.411	20.583	15.574	1.00	49.12	B
ATOM	4299	CA	SER	B	247	36.865	19.894	16.781	1.00	47.41	B
ATOM	4300	CB	SER	B	247	36.242	20.517	18.032	1.00	50.26	B
ATOM	4301	OG	SER	B	247	36.836	21.771	18.313	1.00	55.19	B
ATOM	4302	C	SER	B	247	36.496	18.418	16.700	1.00	46.86	B
ATOM	4303	O	SER	B	247	35.440	18.050	16.181	1.00	48.73	B
ATOM	4304	N	PRO	B	248	37.375	17.544	17.197	1.00	46.53	B
ATOM	4305	CD	PRO	B	248	38.760	17.765	17.663	1.00	43.73	B
ATOM	4306	CA	PRO	B	248	37.064	16.119	17.136	1.00	44.39	B
ATOM	4307	CB	PRO	B	248	38.432	15.468	17.356	1.00	43.90	B
ATOM	4308	CG	PRO	B	248	39.107	16.429	18.284	1.00	41.51	B
ATOM	4309	C	PRO	B	248	36.026	15.664	18.161	1.00	43.34	B
ATOM	4310	O	PRO	B	248	35.758	16.355	19.144	1.00	47.61	B
ATOM	4311	N	GLY	B	249	35.441	14.501	17.904	1.00	40.31	B
ATOM	4312	CA	GLY	B	249	34.472	13.925	18.812	1.00	40.15	B
ATOM	4313	C	GLY	B	249	35.175	12.705	19.381	1.00	42.68	B
ATOM	4314	O	GLY	B	249	36.172	12.255	18.810	1.00	43.39	B
ATOM	4315	N	TYR	B	250	34.676	12.156	20.484	1.00	40.24	B
ATOM	4316	CA	TYR	B	250	35.324	10.999	21.099	1.00	39.41	B
ATOM	4317	CB	TYR	B	250	35.814	11.361	22.505	1.00	41.48	B
ATOM	4318	CG	TYR	B	250	36.633	12.625	22.524	1.00	46.37	B
ATOM	4319	CD1	TYR	B	250	36.044	13.865	22.787	1.00	45.14	B
ATOM	4320	CE1	TYR	B	250	36.784	15.047	22.697	1.00	48.95	B
ATOM	4321	CD2	TYR	B	250	37.984	12.594	22.183	1.00	48.17	B
ATOM	4322	CE2	TYR	B	250	38.729	13.763	22.089	1.00	50.24	B
ATOM	4323	CZ	TYR	B	250	38.128	14.987	22.340	1.00	49.09	B
ATOM	4324	OH	TYR	B	250	38.867	16.146	22.186	1.00	53.93	B
ATOM	4325	C	TYR	B	250	34.440	9.766	21.188	1.00	41.81	B
ATOM	4326	O	TYR	B	250	33.232	9.819	20.934	1.00	43.09	B
ATOM	4327	N	TRP	B	251	35.054	8.645	21.547	1.00	39.81	B
ATOM	4328	CA	TRP	B	251	34.319	7.402	21.679	1.00	39.71	B
ATOM	4329	CB	TRP	B	251	34.172	6.706	20.322	1.00	40.46	B
ATOM	4330	CG	TRP	B	251	35.464	6.505	19.576	1.00	45.50	B
ATOM	4331	CD2	TRP	B	251	35.859	7.169	18.369	1.00	48.00	B
ATOM	4332	CE2	TRP	B	251	37.144	6.682	18.021	1.00	48.29	B
ATOM	4333	CE3	TRP	B	251	35.250	8.131	17.545	1.00	46.11	B
ATOM	4334	CD1	TRP	B	251	36.492	5.664	19.906	1.00	45.18	B
ATOM	4335	NE1	TRP	B	251	37.509	5.765	18.972	1.00	47.11	B

ATOM	4336	CZ2	TRP	B	251	37.831	7.125	16.885	1.00	47.27	B
ATOM	4337	CZ3	TRP	B	251	35.933	8.571	16.415	1.00	48.80	B
ATOM	4338	CH2	TRP	B	251	37.215	8.065	16.096	1.00	48.49	B
ATOM	4339	C	TRP	B	251	34.944	6.443	22.666	1.00	41.98	B
ATOM	4340	O	TRP	B	251	36.172	6.369	22.817	1.00	44.06	B
ATOM	4341	N	HIS	B	252	34.073	5.721	23.354	1.00	38.11	B
ATOM	4342	CA	HIS	B	252	34.481	4.724	24.315	1.00	35.90	B
ATOM	4343	CB	HIS	B	252	33.856	5.027	25.675	1.00	35.64	B
ATOM	4344	CG	HIS	B	252	34.234	4.054	26.747	1.00	33.00	B
ATOM	4345	CD2	HIS	B	252	34.651	2.767	26.680	1.00	36.50	B
ATOM	4346	ND1	HIS	B	252	34.152	4.361	28.088	1.00	37.51	B
ATOM	4347	CE1	HIS	B	252	34.498	3.303	28.802	1.00	39.03	B
ATOM	4348	NE2	HIS	B	252	34.806	2.322	27.971	1.00	39.62	B
ATOM	4349	C	HIS	B	252	33.900	3.470	23.690	1.00	38.33	B
ATOM	4350	O	HIS	B	252	32.698	3.217	23.777	1.00	42.14	B
ATOM	4351	N	VAL	B	253	34.751	2.710	23.011	1.00	36.69	B
ATOM	4352	CA	VAL	B	253	34.303	1.503	22.345	1.00	36.60	B
ATOM	4353	CB	VAL	B	253	34.991	1.328	20.974	1.00	39.98	B
ATOM	4354	CG1	VAL	B	253	34.561	2.445	20.029	1.00	42.45	B
ATOM	4355	CG2	VAL	B	253	36.507	1.337	21.150	1.00	42.35	B
ATOM	4356	C	VAL	B	253	34.556	.257	23.162	1.00	36.72	B
ATOM	4357	O	VAL	B	253	35.446	.217	24.012	1.00	39.21	B
ATOM	4358	N	SER	B	254	33.756	-.765	22.893	1.00	38.25	B
ATOM	4359	CA	SER	B	254	33.887	-2.028	23.587	1.00	40.50	B
ATOM	4360	CB	SER	B	254	33.406	-1.908	25.031	1.00	36.47	B
ATOM	4361	OG	SER	B	254	33.444	-3.186	25.647	1.00	45.21	B
ATOM	4362	C	SER	B	254	33.124	-3.149	22.909	1.00	39.18	B
ATOM	4363	O	SER	B	254	31.924	-3.049	22.656	1.00	41.37	B
ATOM	4364	N	ASN	B	255	33.846	-4.218	22.613	1.00	38.23	B
ATOM	4365	CA	ASN	B	255	33.280	-5.397	21.996	1.00	37.10	B
ATOM	4366	CB	ASN	B	255	32.582	-6.235	23.074	1.00	38.88	B
ATOM	4367	CG	ASN	B	255	32.204	-7.620	22.584	1.00	43.98	B
ATOM	4368	OD1	ASN	B	255	32.874	-8.187	21.716	1.00	46.32	B
ATOM	4369	ND2	ASN	B	255	31.136	-8.181	23.144	1.00	45.47	B
ATOM	4370	C	ASN	B	255	32.345	-5.165	20.815	1.00	38.00	B
ATOM	4371	O	ASN	B	255	31.196	-5.597	20.834	1.00	38.39	B
ATOM	4372	N	ASN	B	256	32.838	-4.481	19.786	1.00	40.17	B
ATOM	4373	CA	ASN	B	256	32.055	-4.263	18.566	1.00	40.45	B
ATOM	4374	CB	ASN	B	256	32.238	-2.841	18.040	1.00	40.14	B
ATOM	4375	CG	ASN	B	256	31.505	-1.814	18.882	1.00	43.75	B
ATOM	4376	OD1	ASN	B	256	30.273	-1.838	18.980	1.00	41.29	B
ATOM	4377	ND2	ASN	B	256	32.253	-.909	19.494	1.00	43.33	B
ATOM	4378	C	ASN	B	256	32.575	-5.275	17.546	1.00	43.15	B
ATOM	4379	O	ASN	B	256	33.758	-5.613	17.557	1.00	45.50	B
ATOM	4380	N	LYS	B	257	31.699	-5.760	16.671	1.00	43.59	B
ATOM	4381	CA	LYS	B	257	32.068	-6.759	15.671	1.00	45.91	B
ATOM	4382	CB	LYS	B	257	31.160	-7.978	15.862	1.00	49.25	B
ATOM	4383	CG	LYS	B	257	31.522	-9.228	15.079	1.00	52.05	B
ATOM	4384	CD	LYS	B	257	30.663	-10.405	15.572	1.00	57.28	B
ATOM	4385	CE	LYS	B	257	31.151	-11.756	15.043	1.00	62.00	B
ATOM	4386	NZ	LYS	B	257	30.798	-12.001	13.602	1.00	64.00	B
ATOM	4387	C	LYS	B	257	31.942	-6.229	14.235	1.00	46.93	B
ATOM	4388	O	LYS	B	257	30.839	-5.895	13.795	1.00	46.62	B
ATOM	4389	N	PHE	B	258	33.061	-6.154	13.507	1.00	45.40	B
ATOM	4390	CA	PHE	B	258	33.049	-5.669	12.122	1.00	42.39	B
ATOM	4391	CB	PHE	B	258	34.208	-4.696	11.888	1.00	40.55	B
ATOM	4392	CG	PHE	B	258	34.303	-3.608	12.917	1.00	40.82	B
ATOM	4393	CD1	PHE	B	258	35.002	-3.817	14.105	1.00	40.62	B
ATOM	4394	CD2	PHE	B	258	33.668	-2.384	12.715	1.00	39.64	B
ATOM	4395	CE1	PHE	B	258	35.071	-2.826	15.082	1.00	42.84	B
ATOM	4396	CE2	PHE	B	258	33.727	-1.381	13.684	1.00	43.11	B
ATOM	4397	CZ	PHE	B	258	34.430	-1.603	14.871	1.00	44.52	B
ATOM	4398	C	PHE	B	258	33.149	-6.834	11.139	1.00	43.66	B
ATOM	4399	O	PHE	B	258	34.078	-7.642	11.218	1.00	48.40	B
ATOM	4400	N	VAL	B	259	32.198	-6.929	10.218	1.00	42.05	B
ATOM	4401	CA	VAL	B	259	32.192	-8.007	9.238	1.00	41.70	B
ATOM	4402	CB	VAL	B	259	30.975	-8.936	9.449	1.00	42.45	B
ATOM	4403	CG1	VAL	B	259	31.004	-10.086	8.441	1.00	40.96	B
ATOM	4404	CG2	VAL	B	259	30.985	-9.488	10.866	1.00	39.91	B

ATOM	4405	C	VAL	B	259	32.150	-7.445	7.822	1.00	45.08	B
ATOM	4406	O	VAL	B	259	31.260	-6.661	7.486	1.00	43.16	B
ATOM	4407	N	ASN	B	260	33.108	-7.862	6.992	1.00	45.64	B
ATOM	4408	CA	ASN	B	260	33.197	-7.393	5.612	1.00	43.81	B
ATOM	4409	CB	ASN	B	260	32.082	-7.993	4.754	1.00	48.98	B
ATOM	4410	CG	ASN	B	260	32.399	-9.402	4.296	1.00	57.52	B
ATOM	4411	OD1	ASN	B	260	33.513	-9.670	3.820	1.00	64.14	B
ATOM	4412	ND2	ASN	B	260	31.425	-10.315	4.425	1.00	55.90	B
ATOM	4413	C	ASN	B	260	33.106	-5.883	5.572	1.00	41.57	B
ATOM	4414	O	ASN	B	260	32.414	-5.311	4.737	1.00	38.20	B
ATOM	4415	N	SER	B	261	33.821	-5.247	6.491	1.00	40.34	B
ATOM	4416	CA	SER	B	261	33.841	-3.797	6.588	1.00	42.65	B
ATOM	4417	CB	SER	B	261	33.377	-3.362	7.987	1.00	43.31	B
ATOM	4418	OG	SER	B	261	32.064	-3.834	8.269	1.00	41.10	B
ATOM	4419	C	SER	B	261	35.260	-3.297	6.322	1.00	45.22	B
ATOM	4420	O	SER	B	261	36.228	-4.047	6.452	1.00	46.15	B
ATOM	4421	N	ARG	B	262	35.381	-2.029	5.946	1.00	48.93	B
ATOM	4422	CA	ARG	B	262	36.684	-1.447	5.655	1.00	51.85	B
ATOM	4423	CB	ARG	B	262	36.999	-1.575	4.159	1.00	57.68	B
ATOM	4424	CG	ARG	B	262	35.814	-1.338	3.232	1.00	67.06	B
ATOM	4425	CD	ARG	B	262	36.299	-.913	1.846	1.00	75.44	B
ATOM	4426	NE	ARG	B	262	36.899	.417	1.912	1.00	87.07	B
ATOM	4427	CZ	ARG	B	262	37.630	.979	.945	1.00	92.99	B
ATOM	4428	NH1	ARG	B	262	38.123	2.204	1.123	1.00	95.56	B
ATOM	4429	NH2	ARG	B	262	37.882	.325	-.191	1.00	95.29	B
ATOM	4430	C	ARG	B	262	36.723	.012	6.067	1.00	49.29	B
ATOM	4431	O	ARG	B	262	35.681	.656	6.201	1.00	52.42	B
ATOM	4432	N	GLY	B	263	37.923	.539	6.261	1.00	45.77	B
ATOM	4433	CA	GLY	B	263	38.045	1.921	6.677	1.00	45.00	B
ATOM	4434	C	GLY	B	263	38.271	2.026	8.172	1.00	45.09	B
ATOM	4435	O	GLY	B	263	38.866	1.136	8.784	1.00	46.40	B
ATOM	4436	N	SER	B	264	37.785	3.112	8.768	1.00	45.85	B
ATOM	4437	CA	SER	B	264	37.957	3.342	10.196	1.00	44.27	B
ATOM	4438	CB	SER	B	264	37.581	4.789	10.519	1.00	42.88	B
ATOM	4439	OG	SER	B	264	37.961	5.136	11.839	1.00	46.51	B
ATOM	4440	C	SER	B	264	37.136	2.363	11.052	1.00	46.54	B
ATOM	4441	O	SER	B	264	35.908	2.346	10.999	1.00	47.16	B
ATOM	4442	N	MET	B	265	37.826	1.538	11.836	1.00	45.27	B
ATOM	4443	CA	MET	B	265	37.175	.560	12.703	1.00	43.71	B
ATOM	4444	CB	MET	B	265	37.218	-.826	12.049	1.00	43.96	B
ATOM	4445	CG	MET	B	265	36.486	-.872	10.723	1.00	45.99	B
ATOM	4446	SD	MET	B	265	36.678	-2.425	9.848	1.00	52.87	B
ATOM	4447	CE	MET	B	265	38.288	-2.153	9.060	1.00	52.47	B
ATOM	4448	C	MET	B	265	37.918	.539	14.028	1.00	41.84	B
ATOM	4449	O	MET	B	265	38.518	-.472	14.401	1.00	44.24	B
ATOM	4450	N	PRO	B	266	37.881	1.664	14.762	1.00	42.11	B
ATOM	4451	CD	PRO	B	266	37.056	2.845	14.451	1.00	42.03	B
ATOM	4452	CA	PRO	B	266	38.553	1.823	16.058	1.00	42.19	B
ATOM	4453	CB	PRO	B	266	38.081	3.201	16.535	1.00	42.20	B
ATOM	4454	CG	PRO	B	266	37.727	3.918	15.255	1.00	43.23	B
ATOM	4455	C	PRO	B	266	38.214	.735	17.070	1.00	46.44	B
ATOM	4456	O	PRO	B	266	37.043	.365	17.218	1.00	46.63	B
ATOM	4457	N	THR	B	267	39.236	.213	17.756	1.00	45.20	B
ATOM	4458	CA	THR	B	267	39.014	-.797	18.788	1.00	46.81	B
ATOM	4459	CB	THR	B	267	39.696	-2.146	18.477	1.00	49.41	B
ATOM	4460	OG1	THR	B	267	41.121	-1.992	18.529	1.00	55.99	B
ATOM	4461	CG2	THR	B	267	39.277	-2.650	17.106	1.00	46.28	B
ATOM	4462	C	THR	B	267	39.589	-.245	20.084	1.00	47.69	B
ATOM	4463	O	THR	B	267	39.554	-.898	21.123	1.00	49.48	B
ATOM	4464	N	THR	B	268	40.122	.972	20.012	1.00	46.80	B
ATOM	4465	CA	THR	B	268	40.684	1.626	21.186	1.00	47.24	B
ATOM	4466	CB	THR	B	268	42.180	1.972	20.982	1.00	49.46	B
ATOM	4467	OG1	THR	B	268	42.369	2.531	19.675	1.00	50.35	B
ATOM	4468	CG2	THR	B	268	43.040	.720	21.112	1.00	49.21	B
ATOM	4469	C	THR	B	268	39.880	2.896	21.422	1.00	46.29	B
ATOM	4470	O	THR	B	268	39.470	3.570	20.471	1.00	46.79	B
ATOM	4471	N	SER	B	269	39.658	3.221	22.688	1.00	46.71	B
ATOM	4472	CA	SER	B	269	38.870	4.396	23.056	1.00	45.08	B
ATOM	4473	CB	SER	B	269	38.174	4.125	24.388	1.00	41.47	B

ATOM	4474	OG	SER	B	269	37.528	2.865	24.343	1.00	45.98	B
ATOM	4475	C	SER	B	269	39.656	5.700	23.145	1.00	42.98	B
ATOM	4476	O	SER	B	269	40.828	5.706	23.516	1.00	47.07	B
ATOM	4477	N	THR	B	270	38.999	6.807	22.806	1.00	41.60	B
ATOM	4478	CA	THR	B	270	39.627	8.120	22.869	1.00	40.04	B
ATOM	4479	CB	THR	B	270	39.483	8.889	21.537	1.00	41.11	B
ATOM	4480	OG1	THR	B	270	38.101	8.962	21.161	1.00	41.09	B
ATOM	4481	CG2	THR	B	270	40.259	8.185	20.432	1.00	38.80	B
ATOM	4482	C	THR	B	270	39.021	8.949	23.999	1.00	41.99	B
ATOM	4483	O	THR	B	270	39.245	10.156	24.090	1.00	41.98	B
ATOM	4484	N	THR	B	271	38.243	8.289	24.855	1.00	42.35	B
ATOM	4485	CA	THR	B	271	37.633	8.945	26.004	1.00	40.99	B
ATOM	4486	CB	THR	B	271	36.570	9.980	25.595	1.00	42.78	B
ATOM	4487	OG1	THR	B	271	36.290	10.840	26.713	1.00	43.61	B
ATOM	4488	CG2	THR	B	271	35.270	9.275	25.185	1.00	42.66	B
ATOM	4489	C	THR	B	271	36.953	7.900	26.862	1.00	41.45	B
ATOM	4490	O	THR	B	271	36.712	6.771	26.418	1.00	44.24	B
ATOM	4491	N	THR	B	272	36.637	8.285	28.092	1.00	43.89	B
ATOM	4492	CA	THR	B	272	35.961	7.393	29.012	1.00	44.80	B
ATOM	4493	CB	THR	B	272	36.704	7.298	30.359	1.00	46.18	B
ATOM	4494	OG1	THR	B	272	37.976	6.669	30.156	1.00	48.66	B
ATOM	4495	CG2	THR	B	272	35.890	6.482	31.364	1.00	46.96	B
ATOM	4496	C	THR	B	272	34.569	7.941	29.263	1.00	44.19	B
ATOM	4497	O	THR	B	272	34.413	9.069	29.738	1.00	47.54	B
ATOM	4498	N	TYR	B	273	33.552	7.160	28.916	1.00	44.99	B
ATOM	4499	CA	TYR	B	273	32.188	7.601	29.156	1.00	41.75	B
ATOM	4500	CB	TYR	B	273	31.582	8.237	27.907	1.00	42.30	B
ATOM	4501	CG	TYR	B	273	30.179	8.740	28.163	1.00	43.35	B
ATOM	4502	CD1	TYR	B	273	29.948	9.772	29.074	1.00	39.85	B
ATOM	4503	CE1	TYR	B	273	28.655	10.178	29.391	1.00	41.66	B
ATOM	4504	CD2	TYR	B	273	29.077	8.128	27.564	1.00	42.79	B
ATOM	4505	CE2	TYR	B	273	27.777	8.526	27.874	1.00	40.62	B
ATOM	4506	CZ	TYR	B	273	27.574	9.546	28.789	1.00	40.66	B
ATOM	4507	OH	TYR	B	273	26.295	9.926	29.121	1.00	41.74	B
ATOM	4508	C	TYR	B	273	31.325	6.444	29.615	1.00	37.63	B
ATOM	4509	O	TYR	B	273	31.253	5.408	28.956	1.00	39.83	B
ATOM	4510	N	ASN	B	274	30.700	6.619	30.774	1.00	40.67	B
ATOM	4511	CA	ASN	B	274	29.818	5.604	31.339	1.00	40.30	B
ATOM	4512	CB	ASN	B	274	30.281	5.197	32.745	1.00	42.59	B
ATOM	4513	CG	ASN	B	274	31.737	4.742	32.779	1.00	46.33	B
ATOM	4514	OD1	ASN	B	274	32.128	3.808	32.065	1.00	47.41	B
ATOM	4515	ND2	ASN	B	274	32.545	5.400	33.606	1.00	42.91	B
ATOM	4516	C	ASN	B	274	28.417	6.198	31.423	1.00	39.60	B
ATOM	4517	O	ASN	B	274	28.193	7.193	32.120	1.00	40.37	B
ATOM	4518	N	PRO	B	275	27.455	5.613	30.693	1.00	38.86	B
ATOM	4519	CD	PRO	B	275	27.566	4.511	29.724	1.00	36.63	B
ATOM	4520	CA	PRO	B	275	26.087	6.136	30.738	1.00	38.65	B
ATOM	4521	CB	PRO	B	275	25.324	5.188	29.819	1.00	35.80	B
ATOM	4522	CG	PRO	B	275	26.371	4.764	28.832	1.00	36.72	B
ATOM	4523	C	PRO	B	275	25.563	6.102	32.174	1.00	39.13	B
ATOM	4524	O	PRO	B	275	25.803	5.145	32.914	1.00	39.91	B
ATOM	4525	N	PRO	B	276	24.852	7.161	32.586	1.00	38.91	B
ATOM	4526	CD	PRO	B	276	24.719	8.419	31.826	1.00	42.08	B
ATOM	4527	CA	PRO	B	276	24.274	7.308	33.919	1.00	37.54	B
ATOM	4528	CB	PRO	B	276	24.048	8.813	34.018	1.00	39.87	B
ATOM	4529	CG	PRO	B	276	23.669	9.166	32.622	1.00	40.32	B
ATOM	4530	C	PRO	B	276	22.992	6.510	34.184	1.00	38.82	B
ATOM	4531	O	PRO	B	276	22.057	7.012	34.810	1.00	38.72	B
ATOM	4532	N	TYR	B	277	22.943	5.273	33.711	1.00	35.95	B
ATOM	4533	CA	TYR	B	277	21.777	4.428	33.947	1.00	35.57	B
ATOM	4534	CB	TYR	B	277	20.649	4.735	32.958	1.00	33.68	B
ATOM	4535	CG	TYR	B	277	21.082	4.827	31.506	1.00	30.14	B
ATOM	4536	CD1	TYR	B	277	21.225	6.069	30.880	1.00	30.71	B
ATOM	4537	CE1	TYR	B	277	21.638	6.165	29.546	1.00	26.68	B
ATOM	4538	CD2	TYR	B	277	21.359	3.678	30.761	1.00	30.15	B
ATOM	4539	CE2	TYR	B	277	21.770	3.765	29.429	1.00	27.70	B
ATOM	4540	CZ	TYR	B	277	21.907	5.014	28.830	1.00	28.37	B
ATOM	4541	OH	TYR	B	277	22.308	5.111	27.513	1.00	30.31	B
ATOM	4542	C	TYR	B	277	22.224	3.002	33.778	1.00	36.64	B

ATOM	4543	O	TYR	B	277	23.281	2.753	33.199	1.00	39.57	B
ATOM	4544	N	SER	B	278	21.443	2.061	34.289	1.00	34.07	B
ATOM	4545	CA	SER	B	278	21.818	.672	34.148	1.00	37.57	B
ATOM	4546	CB	SER	B	278	21.308	-.147	35.336	1.00	35.71	B
ATOM	4547	OG	SER	B	278	19.899	-.270	35.288	1.00	48.95	B
ATOM	4548	C	SER	B	278	21.198	.165	32.854	1.00	36.64	B
ATOM	4549	O	SER	B	278	20.218	.739	32.354	1.00	39.08	B
ATOM	4550	N	TYR	B	279	21.781	-.895	32.310	1.00	35.68	B
ATOM	4551	CA	TYR	B	279	21.293	-1.494	31.080	1.00	35.58	B
ATOM	4552	CB	TYR	B	279	21.653	-.626	29.871	1.00	34.69	B
ATOM	4553	CG	TYR	B	279	23.131	-.352	29.719	1.00	30.53	B
ATOM	4554	CD1	TYR	B	279	23.744	.667	30.441	1.00	31.56	B
ATOM	4555	CE1	TYR	B	279	25.104	.916	30.316	1.00	35.36	B
ATOM	4556	CD2	TYR	B	279	23.921	-1.121	28.862	1.00	34.18	B
ATOM	4557	CE2	TYR	B	279	25.287	-.881	28.733	1.00	30.07	B
ATOM	4558	CZ	TYR	B	279	25.865	.136	29.462	1.00	30.53	B
ATOM	4559	OH	TYR	B	279	27.211	.386	29.347	1.00	40.94	B
ATOM	4560	C	TYR	B	279	21.907	-2.866	30.913	1.00	34.98	B
ATOM	4561	O	TYR	B	279	22.954	-3.163	31.480	1.00	38.78	B
ATOM	4562	N	SER	B	280	21.241	-3.696	30.129	1.00	39.45	B
ATOM	4563	CA	SER	B	280	21.708	-5.047	29.862	1.00	42.48	B
ATOM	4564	CB	SER	B	280	20.532	-6.010	30.015	1.00	42.97	B
ATOM	4565	OG	SER	B	280	19.492	-5.660	29.103	1.00	48.69	B
ATOM	4566	C	SER	B	280	22.233	-5.097	28.424	1.00	41.04	B
ATOM	4567	O	SER	B	280	21.617	-4.512	27.528	1.00	43.32	B
ATOM	4568	N	LEU	B	281	23.360	-5.774	28.198	1.00	40.26	B
ATOM	4569	CA	LEU	B	281	23.922	-5.897	26.850	1.00	37.48	B
ATOM	4570	CB	LEU	B	281	25.414	-5.543	26.843	1.00	37.60	B
ATOM	4571	CG	LEU	B	281	25.812	-4.066	26.933	1.00	37.89	B
ATOM	4572	CD1	LEU	B	281	27.324	-3.950	26.914	1.00	38.66	B
ATOM	4573	CD2	LEU	B	281	25.218	-3.295	25.768	1.00	38.71	B
ATOM	4574	C	LEU	B	281	23.754	-7.308	26.305	1.00	38.63	B
ATOM	4575	O	LEU	B	281	24.116	-8.279	26.972	1.00	42.02	B
ATOM	4576	N	ASP	B	282	23.188	-7.425	25.110	1.00	35.10	B
ATOM	4577	CA	ASP	B	282	23.028	-8.728	24.469	1.00	37.91	B
ATOM	4578	CB	ASP	B	282	22.004	-8.669	23.329	1.00	35.67	B
ATOM	4579	CG	ASP	B	282	20.575	-8.581	23.824	1.00	38.93	B
ATOM	4580	OD1	ASP	B	282	20.199	-9.370	24.715	1.00	41.42	B
ATOM	4581	OD2	ASP	B	282	19.817	-7.734	23.316	1.00	37.98	B
ATOM	4582	C	ASP	B	282	24.388	-9.099	23.881	1.00	40.25	B
ATOM	4583	O	ASP	B	282	25.204	-8.221	23.593	1.00	42.46	B
ATOM	4584	N	ASN	B	283	24.630	-10.393	23.706	1.00	41.62	B
ATOM	4585	CA	ASN	B	283	25.885	-10.872	23.129	1.00	41.25	B
ATOM	4586	CB	ASN	B	283	25.884	-12.409	23.081	1.00	45.43	B
ATOM	4587	CG	ASN	B	283	27.184	-12.987	22.528	1.00	49.61	B
ATOM	4588	OD1	ASN	B	283	27.801	-12.424	21.617	1.00	52.33	B
ATOM	4589	ND2	ASN	B	283	27.598	-14.132	23.071	1.00	59.46	B
ATOM	4590	C	ASN	B	283	25.962	-10.310	21.706	1.00	40.54	B
ATOM	4591	O	ASN	B	283	24.984	-10.385	20.957	1.00	39.53	B
ATOM	4592	N	VAL	B	284	27.118	-9.768	21.328	1.00	38.10	B
ATOM	4593	CA	VAL	B	284	27.265	-9.194	19.998	1.00	39.54	B
ATOM	4594	CB	VAL	B	284	28.693	-8.658	19.775	1.00	39.37	B
ATOM	4595	CG1	VAL	B	284	29.671	-9.811	19.614	1.00	38.66	B
ATOM	4596	CG2	VAL	B	284	28.707	-7.734	18.560	1.00	43.55	B
ATOM	4597	C	VAL	B	284	26.912	-10.193	18.899	1.00	40.12	B
ATOM	4598	O	VAL	B	284	26.458	-9.812	17.822	1.00	38.06	B
ATOM	4599	N	ASP	B	285	27.106	-11.477	19.181	1.00	40.23	B
ATOM	4600	CA	ASP	B	285	26.800	-12.522	18.209	1.00	42.50	B
ATOM	4601	CB	ASP	B	285	27.468	-13.840	18.609	1.00	49.23	B
ATOM	4602	CG	ASP	B	285	28.893	-13.932	18.133	1.00	52.34	B
ATOM	4603	OD1	ASP	B	285	29.765	-13.249	18.706	1.00	51.42	B
ATOM	4604	OD2	ASP	B	285	29.133	-14.690	17.166	1.00	59.38	B
ATOM	4605	C	ASP	B	285	25.312	-12.769	18.029	1.00	41.41	B
ATOM	4606	O	ASP	B	285	24.904	-13.392	17.039	1.00	40.03	B
ATOM	4607	N	ASN	B	286	24.508	-12.301	18.987	1.00	39.96	B
ATOM	4608	CA	ASN	B	286	23.054	-12.485	18.926	1.00	40.98	B
ATOM	4609	CB	ASN	B	286	22.498	-12.758	20.331	1.00	44.72	B
ATOM	4610	CG	ASN	B	286	23.007	-14.068	20.931	1.00	49.13	B
ATOM	4611	OD1	ASN	B	286	23.173	-14.178	22.154	1.00	52.22	B

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ATOM   4612  ND2 ASN B 286      23.239 -15.069  20.083  1.00 49.87      B
ATOM   4613  C   ASN B 286      22.303 -11.280  18.334  1.00 39.99      B
ATOM   4614  O   ASN B 286      21.140 -11.395  17.941  1.00 40.31      B
ATOM   4615  N   VAL B 287      22.977 -10.137  18.265  1.00 37.31      B
ATOM   4616  CA  VAL B 287      22.383  -8.895  17.770  1.00 37.49      B
ATOM   4617  CB  VAL B 287      23.462  -7.794  17.634  1.00 37.03      B
ATOM   4618  CG1 VAL B 287      22.879  -6.561  16.946  1.00 37.73      B
ATOM   4619  CG2 VAL B 287      24.000  -7.431  19.008  1.00 35.14      B
ATOM   4620  C   VAL B 287      21.605  -8.965  16.464  1.00 37.17      B
ATOM   4621  O   VAL B 287      20.444  -8.562  16.402  1.00 36.15      B
ATOM   4622  N   LYS B 288      22.250  -9.459  15.418  1.00 33.47      B
ATOM   4623  CA  LYS B 288      21.604  -9.549  14.118  1.00 35.81      B
ATOM   4624  CB  LYS B 288      22.506 -10.302  13.133  1.00 33.48      B
ATOM   4625  CG  LYS B 288      21.982 -10.338  11.705  1.00 37.23      B
ATOM   4626  CD  LYS B 288      23.048 -10.874  10.757  1.00 40.09      B
ATOM   4627  CE  LYS B 288      22.547 -10.928   9.327  1.00 42.70      B
ATOM   4628  NZ  LYS B 288      23.613 -11.442   8.425  1.00 47.13      B
ATOM   4629  C   LYS B 288      20.256 -10.237  14.209  1.00 34.98      B
ATOM   4630  O   LYS B 288      19.233  -9.682  13.811  1.00 37.78      B
ATOM   4631  N   SER B 289      20.265 -11.452  14.741  1.00 34.22      B
ATOM   4632  CA  SER B 289      19.057 -12.252  14.874  1.00 33.34      B
ATOM   4633  CB  SER B 289      19.416 -13.601  15.512  1.00 35.25      B
ATOM   4634  OG  SER B 289      18.266 -14.397  15.690  1.00 39.92      B
ATOM   4635  C   SER B 289      17.946 -11.576  15.683  1.00 31.86      B
ATOM   4636  O   SER B 289      16.777 -11.591  15.288  1.00 31.07      B
ATOM   4637  N   ILE B 290      18.313 -10.986  16.814  1.00 30.63      B
ATOM   4638  CA  ILE B 290      17.328 -10.339  17.677  1.00 32.84      B
ATOM   4639  CB  ILE B 290      17.944  -9.983  19.039  1.00 31.20      B
ATOM   4640  CG2 ILE B 290      16.956  -9.165  19.865  1.00 36.60      B
ATOM   4641  CG1 ILE B 290      18.305 -11.273  19.783  1.00 37.83      B
ATOM   4642  CD1 ILE B 290      19.050 -11.049  21.092  1.00 33.75      B
ATOM   4643  C   ILE B 290      16.716  -9.092  17.065  1.00 31.00      B
ATOM   4644  O   ILE B 290      15.501  -8.912  17.097  1.00 32.04      B
ATOM   4645  N   VAL B 291      17.563  -8.244  16.490  1.00 29.00      B
ATOM   4646  CA  VAL B 291      17.108  -7.003  15.874  1.00 30.08      B
ATOM   4647  CB  VAL B 291      18.312  -6.082  15.563  1.00 27.81      B
ATOM   4648  CG1 VAL B 291      17.863  -4.853  14.773  1.00 28.89      B
ATOM   4649  CG2 VAL B 291      18.968  -5.656  16.862  1.00 27.40      B
ATOM   4650  C   VAL B 291      16.278  -7.224  14.610  1.00 28.72      B
ATOM   4651  O   VAL B 291      15.193  -6.661  14.479  1.00 27.15      B
ATOM   4652  N   LYS B 292      16.773  -8.054  13.694  1.00 31.12      B
ATOM   4653  CA  LYS B 292      16.053  -8.316  12.453  1.00 34.72      B
ATOM   4654  CB  LYS B 292      16.847  -9.275  11.554  1.00 34.68      B
ATOM   4655  CG  LYS B 292      18.173  -8.709  11.077  1.00 31.47      B
ATOM   4656  CD  LYS B 292      18.797  -9.566   9.985  1.00 39.29      B
ATOM   4657  CE  LYS B 292      18.013  -9.485   8.674  1.00 41.18      B
ATOM   4658  NZ  LYS B 292      18.633 -10.343   7.620  1.00 42.61      B
ATOM   4659  C   LYS B 292      14.653  -8.878  12.681  1.00 34.74      B
ATOM   4660  O   LYS B 292      13.723  -8.576  11.929  1.00 36.49      B
ATOM   4661  N   GLN B 293      14.493  -9.687  13.721  1.00 31.80      B
ATOM   4662  CA  GLN B 293      13.188 -10.279  13.999  1.00 35.63      B
ATOM   4663  CB  GLN B 293      13.357 -11.642  14.670  1.00 38.14      B
ATOM   4664  CG  GLN B 293      13.947 -12.709  13.762  1.00 50.41      B
ATOM   4665  CD  GLN B 293      13.994 -14.068  14.437  1.00 56.39      B
ATOM   4666  OE1 GLN B 293      14.360 -15.079  13.821  1.00 59.25      B
ATOM   4667  NE2 GLN B 293      13.620 -14.103  15.715  1.00 60.94      B
ATOM   4668  C   GLN B 293      12.252  -9.443  14.858  1.00 29.05      B
ATOM   4669  O   GLN B 293      11.035  -9.584  14.762  1.00 31.94      B
ATOM   4670  N   ASN B 294      12.805  -8.564  15.686  1.00 29.40      B
ATOM   4671  CA  ASN B 294      11.961  -7.769  16.578  1.00 31.65      B
ATOM   4672  CB  ASN B 294      12.352  -8.077  18.032  1.00 31.69      B
ATOM   4673  CG  ASN B 294      12.124  -9.536  18.395  1.00 32.72      B
ATOM   4674  OD1 ASN B 294      10.991  -9.970  18.593  1.00 36.23      B
ATOM   4675  ND2 ASN B 294      13.200 -10.302  18.463  1.00 32.81      B
ATOM   4676  C   ASN B 294      11.884  -6.250  16.372  1.00 33.15      B
ATOM   4677  O   ASN B 294      11.122  -5.574  17.062  1.00 32.50      B
ATOM   4678  N   ALA B 295      12.654  -5.706  15.436  1.00 29.61      B
ATOM   4679  CA  ALA B 295      12.609  -4.260  15.197  1.00 32.24      B
ATOM   4680  CB  ALA B 295      13.991  -3.744  14.802  1.00 27.12      B
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ATOM	4681	C	ALA	B	295	11.591	-3.916	14.113	1.00	26.47	B
ATOM	4682	O	ALA	B	295	11.181	-4.778	13.352	1.00	26.78	B
ATOM	4683	N	GLY	B	296	11.184	-2.653	14.046	1.00	26.86	B
ATOM	4684	CA	GLY	B	296	10.232	-2.250	13.030	1.00	22.95	B
ATOM	4685	C	GLY	B	296	8.786	-2.305	13.476	1.00	27.36	B
ATOM	4686	O	GLY	B	296	8.497	-2.520	14.653	1.00	26.93	B
ATOM	4687	N	VAL	B	297	7.877	-2.122	12.522	1.00	28.99	B
ATOM	4688	CA	VAL	B	297	6.447	-2.115	12.799	1.00	27.48	B
ATOM	4689	CB	VAL	B	297	5.681	-1.268	11.753	1.00	29.25	B
ATOM	4690	CG1	VAL	B	297	6.278	.134	11.677	1.00	27.94	B
ATOM	4691	CG2	VAL	B	297	5.730	-1.941	10.401	1.00	28.98	B
ATOM	4692	C	VAL	B	297	5.835	-3.502	12.831	1.00	29.57	B
ATOM	4693	O	VAL	B	297	6.377	-4.441	12.254	1.00	28.97	B
ATOM	4694	N	GLY	B	298	4.701	-3.616	13.514	1.00	30.32	B
ATOM	4695	CA	GLY	B	298	4.012	-4.888	13.617	1.00	30.14	B
ATOM	4696	C	GLY	B	298	4.602	-5.876	14.609	1.00	30.49	B
ATOM	4697	O	GLY	B	298	4.162	-7.020	14.663	1.00	35.29	B
ATOM	4698	N	LYS	B	299	5.584	-5.457	15.399	1.00	28.92	B
ATOM	4699	CA	LYS	B	299	6.205	-6.355	16.377	1.00	32.64	B
ATOM	4700	CB	LYS	B	299	7.717	-6.128	16.423	1.00	32.78	B
ATOM	4701	CG	LYS	B	299	8.406	-6.277	15.073	1.00	36.96	B
ATOM	4702	CD	LYS	B	299	8.071	-7.609	14.422	1.00	39.65	B
ATOM	4703	CE	LYS	B	299	8.889	-7.824	13.162	1.00	44.84	B
ATOM	4704	NZ	LYS	B	299	8.722	-6.678	12.228	1.00	52.50	B
ATOM	4705	C	LYS	B	299	5.642	-6.171	17.780	1.00	37.01	B
ATOM	4706	O	LYS	B	299	5.616	-7.104	18.587	1.00	39.06	B
ATOM	4707	N	ILE	B	300	5.245	-4.940	18.077	1.00	33.48	B
ATOM	4708	CA	ILE	B	300	4.672	-4.614	19.364	1.00	32.65	B
ATOM	4709	CB	ILE	B	300	5.368	-3.385	20.000	1.00	33.88	B
ATOM	4710	CG2	ILE	B	300	4.959	-2.102	19.271	1.00	31.57	B
ATOM	4711	CG1	ILE	B	300	5.035	-3.326	21.492	1.00	32.78	B
ATOM	4712	CD1	ILE	B	300	5.770	-2.221	22.263	1.00	34.92	B
ATOM	4713	C	ILE	B	300	3.230	-4.315	19.021	1.00	34.07	B
ATOM	4714	O	ILE	B	300	2.936	-3.876	17.910	1.00	35.50	B
ATOM	4715	N	ASN	B	301	2.325	-4.578	19.952	1.00	36.43	B
ATOM	4716	CA	ASN	B	301	.908	-4.360	19.697	1.00	37.69	B
ATOM	4717	CB	ASN	B	301	.200	-5.714	19.688	1.00	41.10	B
ATOM	4718	CG	ASN	B	301	-1.245	-5.617	19.237	1.00	51.66	B
ATOM	4719	OD1	ASN	B	301	-1.607	-4.746	18.429	1.00	54.84	B
ATOM	4720	ND2	ASN	B	301	-2.082	-6.529	19.737	1.00	50.14	B
ATOM	4721	C	ASN	B	301	.322	-3.429	20.755	1.00	39.48	B
ATOM	4722	O	ASN	B	301	-.289	-3.875	21.728	1.00	37.48	B
ATOM	4723	N	PRO	B	302	.488	-2.110	20.559	1.00	40.73	B
ATOM	4724	CD	PRO	B	302	1.029	-1.499	19.328	1.00	40.86	B
ATOM	4725	CA	PRO	B	302	.000	-1.073	21.481	1.00	40.71	B
ATOM	4726	CB	PRO	B	302	.553	.215	20.873	1.00	41.26	B
ATOM	4727	CG	PRO	B	302	.502	-.070	19.414	1.00	43.77	B
ATOM	4728	C	PRO	B	302	-1.506	-1.016	21.691	1.00	38.41	B
ATOM	4729	O	PRO	B	302	-2.245	-1.708	20.971	1.00	44.11	B
ATOM	4730	OXT	PRO	B	302	-1.931	-.274	22.591	1.00	43.96	B
ATOM	4731	OH2	WAT	S	401	-11.750	12.515	44.697	1.00	25.85	S
ATOM	4732	OH2	WAT	S	402	10.987	1.222	45.619	1.00	24.63	S
ATOM	4733	OH2	WAT	S	403	9.466	6.037	43.648	1.00	22.40	S
ATOM	4734	OH2	WAT	S	404	1.131	21.494	57.675	1.00	29.33	S
ATOM	4735	OH2	WAT	S	405	2.874	15.130	62.238	1.00	38.91	S
ATOM	4736	OH2	WAT	S	406	-12.592	21.435	53.767	1.00	31.01	S
ATOM	4737	OH2	WAT	S	407	8.446	9.893	37.634	1.00	19.87	S
ATOM	4738	OH2	WAT	S	408	15.523	-3.843	57.406	1.00	30.07	S
ATOM	4739	OH2	WAT	S	409	7.927	2.957	42.152	1.00	27.62	S
ATOM	4740	OH2	WAT	S	410	1.896	10.853	65.930	1.00	43.53	S
ATOM	4741	OH2	WAT	S	411	-8.909	3.441	37.533	1.00	44.45	S
ATOM	4742	OH2	WAT	S	412	-6.954	6.113	36.041	1.00	40.90	S
ATOM	4743	OH2	WAT	S	413	16.258	10.679	37.198	1.00	41.54	S
ATOM	4744	OH2	WAT	S	414	34.865	-1.182	18.586	1.00	42.44	S
ATOM	4745	OH2	WAT	S	415	13.935	1.270	25.171	1.00	27.12	S
ATOM	4746	OH2	WAT	S	416	25.372	16.529	13.482	1.00	44.73	S
ATOM	4747	OH2	WAT	S	417	20.232	13.536	8.421	1.00	30.76	S
ATOM	4748	OH2	WAT	S	418	17.875	2.324	31.580	1.00	36.96	S
ATOM	4749	OH2	WAT	S	419	1.629	.338	11.981	1.00	25.62	S

ATOM	4750	OH2	WAT	S	420	14.065	-2.536	25.280	1.00	32.93	S
ATOM	4751	OH2	WAT	S	421	18.233	10.994	3.179	1.00	39.45	S
ATOM	4752	OH2	WAT	S	422	12.098	5.858	34.422	1.00	44.34	S
ATOM	4753	OH2	WAT	S	423	1.252	9.526	30.732	1.00	27.03	S
ATOM	4754	OH2	WAT	S	424	6.213	-2.784	16.279	1.00	27.86	S
ATOM	4755	OH2	WAT	S	425	2.742	-5.552	22.558	1.00	25.37	S
ATOM	4756	OH2	WAT	S	426	-10.043	23.324	48.325	1.00	25.31	S
ATOM	4757	OH2	WAT	S	427	-4.322	18.521	59.359	1.00	22.03	S
ATOM	4758	OH2	WAT	S	428	-5.613	15.702	58.664	1.00	24.91	S
ATOM	4759	OH2	WAT	S	429	4.351	21.755	51.908	1.00	25.12	S
ATOM	4760	OH2	WAT	S	430	-8.948	26.307	56.612	1.00	24.70	S
ATOM	4761	OH2	WAT	S	431	13.804	9.120	36.281	1.00	30.94	S
ATOM	4762	OH2	WAT	S	432	1.017	20.600	11.654	1.00	29.30	S
ATOM	4763	OH2	WAT	S	433	-8.314	16.742	62.427	1.00	30.20	S
ATOM	4764	OH2	WAT	S	434	-10.434	27.572	43.316	1.00	23.61	S
ATOM	4765	OH2	WAT	S	435	9.369	12.910	32.772	1.00	31.28	S
ATOM	4766	OH2	WAT	S	436	-6.513	-4.271	45.301	1.00	31.36	S
ATOM	4767	OH2	WAT	S	437	-7.896	-1.162	45.723	1.00	32.21	S
ATOM	4768	OH2	WAT	S	438	-.454	19.247	26.874	1.00	32.26	S
ATOM	4769	OH2	WAT	S	439	-8.120	25.535	37.331	1.00	30.49	S
ATOM	4770	OH2	WAT	S	440	-8.701	21.106	37.622	1.00	31.00	S
ATOM	4771	OH2	WAT	S	441	20.497	16.399	28.741	1.00	38.69	S
ATOM	4772	OH2	WAT	S	442	5.134	15.588	31.740	1.00	31.38	S
ATOM	4773	OH2	WAT	S	443	19.347	17.963	-7.503	1.00	33.93	S
ATOM	4774	OH2	WAT	S	444	.631	23.120	63.096	1.00	32.54	S
ATOM	4775	OH2	WAT	S	445	-8.887	33.816	53.878	1.00	31.07	S
ATOM	4776	OH2	WAT	S	446	-12.870	10.958	42.409	1.00	34.92	S
ATOM	4777	OH2	WAT	S	447	-2.276	21.778	62.383	1.00	44.32	S
ATOM	4778	OH2	WAT	S	448	11.396	-3.355	51.760	1.00	31.79	S
ATOM	4779	OH2	WAT	S	449	6.821	-3.277	56.969	1.00	30.84	S
ATOM	4780	OH2	WAT	S	450	19.215	-2.687	27.266	1.00	39.65	S
ATOM	4781	OH2	WAT	S	451	4.122	5.310	39.119	1.00	36.05	S
ATOM	4782	OH2	WAT	S	452	13.695	13.039	64.251	1.00	36.09	S
ATOM	4783	OH2	WAT	S	453	2.025	5.072	24.775	1.00	38.96	S
ATOM	4784	OH2	WAT	S	454	8.976	-2.693	9.885	1.00	35.02	S
ATOM	4785	OH2	WAT	S	455	9.614	16.877	10.320	1.00	39.86	S
ATOM	4786	OH2	WAT	S	456	-6.369	25.665	54.931	1.00	30.78	S
ATOM	4787	OH2	WAT	S	457	17.758	12.392	-.971	1.00	31.25	S
ATOM	4788	OH2	WAT	S	458	1.159	26.402	46.053	1.00	34.49	S
ATOM	4789	OH2	WAT	S	459	11.016	8.326	37.212	1.00	32.48	S
ATOM	4790	OH2	WAT	S	460	7.280	3.807	29.910	1.00	32.47	S
ATOM	4791	OH2	WAT	S	461	-9.819	30.235	47.466	1.00	42.52	S
ATOM	4792	OH2	WAT	S	462	6.743	16.975	6.032	1.00	37.75	S
ATOM	4793	OH2	WAT	S	463	-9.470	14.089	15.217	1.00	35.18	S
ATOM	4794	OH2	WAT	S	464	28.698	9.401	8.858	1.00	35.30	S
ATOM	4795	OH2	WAT	S	465	-10.307	26.490	53.584	1.00	32.14	S
ATOM	4796	OH2	WAT	S	466	-1.219	16.252	30.116	1.00	33.00	S
ATOM	4797	OH2	WAT	S	467	24.138	15.678	19.946	1.00	38.81	S
ATOM	4798	OH2	WAT	S	468	16.335	3.289	-2.318	1.00	38.94	S
ATOM	4799	OH2	WAT	S	469	17.470	9.860	.545	1.00	32.99	S
ATOM	4800	OH2	WAT	S	470	12.107	18.559	11.019	1.00	38.55	S
ATOM	4801	OH2	WAT	S	471	29.987	12.846	47.891	1.00	41.32	S
ATOM	4802	OH2	WAT	S	472	2.660	13.724	33.428	1.00	37.68	S
ATOM	4803	OH2	WAT	S	473	19.495	16.945	7.899	1.00	35.57	S
ATOM	4804	OH2	WAT	S	474	-7.220	20.220	11.588	1.00	38.76	S
ATOM	4805	OH2	WAT	S	475	9.562	5.561	32.540	1.00	33.96	S
ATOM	4806	OH2	WAT	S	476	3.810	-1.987	39.076	1.00	39.27	S
ATOM	4807	OH2	WAT	S	477	-1.498	28.684	45.015	1.00	42.18	S
ATOM	4808	OH2	WAT	S	478	-5.580	30.392	49.014	1.00	34.69	S
ATOM	4809	OH2	WAT	S	479	-6.821	9.283	37.070	1.00	42.28	S
ATOM	4810	OH2	WAT	S	480	-8.091	15.942	4.774	1.00	34.18	S
ATOM	4811	OH2	WAT	S	481	-5.203	20.698	9.215	1.00	45.51	S
ATOM	4812	OH2	WAT	S	482	12.641	15.986	63.366	1.00	50.35	S
ATOM	4813	OH2	WAT	S	483	8.089	7.355	34.551	1.00	45.18	S
ATOM	4814	OH2	WAT	S	484	10.667	23.250	44.693	1.00	42.99	S
ATOM	4815	OH2	WAT	S	485	6.100	26.270	40.709	1.00	40.98	S
ATOM	4817	OH2	WAT	S	486	9.024	17.811	7.630	1.00	30.45	S
ATOM	4818	OH2	WAT	S	487	-2.151	2.277	6.365	1.00	40.14	S
ATOM	4820	OH2	WAT	S	488	-1.797	12.110	34.448	1.00	40.12	S

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ATOM   4821  OH2 WAT S 489      -7.803  15.695  35.223  1.00 38.83      S
ATOM   4822  OH2 WAT S 490       1.261   9.154  68.501  1.00 44.44      S
ATOM   4823  OH2 WAT S 491     -16.715  17.531  56.527  1.00 39.19      S
ATOM   4824  OH2 WAT S 492      -7.615  15.242   -.845  1.00 40.41      S
ATOM   4825  OH2 WAT S 493      11.124   7.721  -3.504  1.00 41.03      S
ATOM   4826  OH2 WAT S 494      28.570  12.642   8.963  1.00 38.21      S
ATOM   4827  OH2 WAT S 495     -16.327   6.334  45.573  1.00 36.44      S
ATOM   4828  OH2 WAT S 496       1.752  12.397    .135  1.00 44.36      S
ATOM   4829  OH2 WAT S 497      -4.224  34.457  54.927  1.00 50.16      S
ATOM   4830  OH2 WAT S 498      24.987 -10.770  15.393  1.00 43.14      S
ATOM   4831  OH2 WAT S 499       9.896  21.920  26.320  1.00 40.20      S
ATOM   4832  OH2 WAT S 500      20.738  18.099   5.291  1.00 37.44      S
ATOM   4833  OH2 WAT S 501      25.669   8.526  44.685  1.00 38.07      S
ATOM   4834  OH2 WAT S 502      -7.682  15.395  21.236  1.00 44.67      S
ATOM   4836  OH2 WAT S 503      13.964   6.330  38.134  1.00 36.32      S
ATOM   4837  OH2 WAT S 504      -7.818  22.802   6.914  1.00 41.83      S
ATOM   4838  OH2 WAT S 505       2.160   2.452  23.162  1.00 34.49      S
ATOM   4839  OH2 WAT S 506      30.392  10.549   4.719  1.00 44.25      S
ATOM   4840  OH2 WAT S 507      28.185  13.556   6.056  1.00 46.45      S
ATOM   4841  OH2 WAT S 508      -3.014  31.738  60.172  1.00 42.95      S
ATOM   4842  OH2 WAT S 509      15.673  20.885  27.163  1.00 43.89      S
ATOM   4843  OH2 WAT S 510      -4.796  36.110  57.454  1.00 31.51      S
ATOM   4844  OH2 WAT S 511       4.313  27.477  47.882  1.00 40.59      S
ATOM   4845  OH2 WAT S 512      -1.721   2.135  68.496  1.00 42.59      S
ATOM   4846  OH2 WAT S 513      -4.402   7.277  27.308  1.00 44.52      S
ATOM   4847  OH2 WAT S 514       6.724   2.355   -.419  1.00 46.97      S
ATOM   4848  OH2 WAT S 515      15.220   3.843  40.270  1.00 42.38      S
ATOM   4849  OH2 WAT S 516      25.445  13.797  59.234  1.00 46.80      S
ATOM   4850  OH2 WAT S 517      12.636   3.242  -1.066  1.00 45.33      S
ATOM   4851  OH2 WAT S 518      28.308  23.795  10.419  1.00 48.96      S
ATOM   4852  OH2 WAT S 519      -2.937  20.555  25.346  1.00 43.81      S
ATOM   4853  OH2 WAT S 520        .865  -4.036  15.946  1.00 47.61      S
ATOM   4854  OH2 WAT S 521      -3.357  -1.792  37.609  1.00 40.58      S
ATOM   4855  OH2 WAT S 522      10.366  21.836   1.462  1.00 42.77      S
ATOM   4856  OH2 WAT S 523      21.224   3.386  47.475  1.00 41.44      S
ATOM   4857  OH2 WAT S 524       5.865   5.506  35.555  1.00 42.87      S
ATOM   4858  OH2 WAT S 525       1.205  16.220  34.544  1.00 44.14      S
ATOM   4859  OH2 WAT S 526       5.909  -4.202  63.229  1.00 50.10      S
ATOM   4860  OH2 WAT S 527      -2.717  21.564  22.414  1.00 40.90      S
ATOM   4861  OH2 WAT S 528      21.869 -12.021  23.977  1.00 49.07      S
ATOM   4862  OH2 WAT S 529      20.613  26.489  57.602  1.00 42.65      S
ATOM   4863  OH2 WAT S 530      25.175  11.833   2.487  1.00 48.87      S
ATOM   4864  OH2 WAT S 531     -11.450  14.722  37.554  1.00 49.87      S
ATOM   4865  OH2 WAT S 532     -12.913  11.860  64.639  1.00 43.89      S
ATOM   4866  OH2 WAT S 533     -13.578   7.901  62.735  1.00 44.04      S
ATOM   4867  OH2 WAT S 534      16.785 -10.543  57.656  1.00 41.95      S
ATOM   4868  OH2 WAT S 535      14.649    .676  42.638  1.00 44.46      S
ATOM   4869  OH2 WAT S 536      -4.111  14.068  65.843  1.00 44.77      S
ATOM   4870  OH2 WAT S 537      -4.342  18.183  62.690  1.00 46.79      S
ATOM   4871  OH2 WAT S 538       5.178  22.956  38.816  1.00 46.79      S
ATOM   4872  OH2 WAT S 539      15.240  12.993  -7.600  1.00 45.03      S
ATOM   4873  OH2 WAT S 540       1.731  10.696  71.024  1.00 50.10      S
ATOM   4874  OH2 WAT S 541      16.873  15.789  36.268  1.00 48.75      S
ATOM   4875  OH2 WAT S 542      22.788  26.946  14.334  1.00 46.72      S
ATOM   4876 SR+2 SR2   398       7.687  17.354  64.118   .43 39.26      AC1
ATOM   4877 SR+2 SR2   399      16.738  17.935   8.716   .36 31.64      AC1
ATOM   4878 SR+2 SR2   398       8.695  17.086  66.181   .54 36.65      AC2
ATOM   4879 SR+2 SR2   399      15.519  18.943   7.336   .64 31.33      AC2
END
```

CLAIMS

1. A variant of a wild-type parent pectate lyase (EC 4.2.2.2) having the conserved amino acid residues D111, D141 or E141, D145, K165, R194 and R199 when aligned with the pectate lyase comprising the amino acid sequence of SEQ ID NO: 2, in which the variant is substituted in at least one position selected from the group consisting of the positions 5, 8, 9, 10, 19, 38, 39, 40, 41, 55, 56, 59, 61, 64, 71, 72, 82, 83, 90, 100, 102, 109, 112, 114, 117, 129, 133, 136, 137, 139, 142, 144, 160, 163, 164, 66, 167, 168, 169, 171, 173, 179, 189, 192, 197, 198, 200, 203, 207, 214, 220, 222, 224, 230, 232, 236, 237, 238, 244, 246, 261, 262, 264, 265, 266, 269, 278, 282, 283, 284, 285, 288, 289 and 297.

2. The variant according to claim 1, which is derived from a wild-type variant holding the conserved amino acid residues W123, D125 and H126.

3. The variant according to claim 1 comprising at least one substituted amino acid residue selected from the group consisting of A41P, T55P, V71N, S72I,T, L82I, K83N,H, W90H, L100N, I102F, G114N, L129F, L133N, D136A,P,S,T,V, F144V, V160F, G163L,H,I, M167F,I,S, L168N, M169I, E189H,N, N192Y, S197N, F198V, F200N,Y, G203V,A, N207S, S220,V, M222N,Y, N230E, L232N, A236V, K237N, D238N, Y244D, S246R,P, S261I, R262E, M265K, S269P, D282H, N283P, D284P, D285G, K288P and S289P.

4. The variant according to claim 1 comprising the amino acid sequence of SEQ ID NO: 7.

5. The variant according to claim 1 comprising the amino acid sequence of SEQ ID NO: 8.

6. The variant according to claim 4 comprising one of the following substitutions:

M169I + F198V + E189H

M169I + F198V + S72I

M169I + F198V + F144V + M167I

7. The variant according to claim 5 comprising one of the following substitutions:

M169I + F198V + S72I + M265K
M169I + F198V + S72I + G203V
M169I + F198V + S72I + K83H

8. The variant according to claim 4 comprising one of the following substitutions:

M169I + F198V + S72T
M169I + F198V + M167I
M169I + F198V + S72I + L82I + I102F + L129F + V160F

9. The variant according to claim 3 comprising one of the following substitutions:

N207S
N230E
N207S + N230E
M169I + F198V + V71N
M169I + F198V + W90H
M169I + F198V + L100N
M169I + F198V + S72I + W90H
M169I + F198V + S72I + G163I
M169I + F198V + S72I + G203A
M169I + F198V + S72I + F144V + M167S
M169I + F198V + S72I + G163I + A236V + S261I

10. The variant according to claim 1 comprising one of the following substitutions:

M169I + F198V + T55P
M169I + F198V + S269P
D282H + N283P + D284P
D282H + N283P + D284P + K288P
M169I + F198V + N283P + D284P + K288P + S289P

11. The variant according to claim 1 comprising one of the following substitutions:

M169I + F198V + A41P
M169I + F198V + D136P
M169I + F198V + N283P
N283P + D285G

12. The variant according to claim 1 comprising one of the following substitutions:
M169I + F198V + D136S
M169I + F198V + D136T
M169I + F198V + S72I + M265K
M169I + F198V + S72I + K83N

13. The variant according to claim 1 comprising one of the following substitutions:
R262T
K237N + D238N
K237N + D238N + R262T
Y244D + S246R
N283P + D285G

14. An isolated polynucleotide molecule encoding the pectate lyase variant according to claim 1, which molecule is prepared from the molecule comprising the DNA sequence of SEQ ID NO:1 by conventional methods such as site-directed mutagenesis.

15. An expression vector comprising the following operably linked elements: (a) a transcription promoter, (b) the polynucleotide molecule of claim 6, and (c) degenerate nucleotide sequences of (a) or (b); and a transcription terminator.

16. A cultured cell into which has been introduced an expression vector according to claim 14, wherein said cell expresses the polypeptide encoded by the DNA segment.

17. A method of producing a polypeptide having pectate lyase activity comprising culturing a cell into which has been introduced an expression vector according to claim 14, whereby

said cell expresses a polypeptide encoded by the DNA segment; and recovering the polypeptide.

18. An enzyme preparation comprising the pectate lyase variant according to claim 1.

19. The preparation according to claim 18 which further comprises one or more enzymes selected from the group consisting of proteases, cellulases (endoglucanases), β-glucanases, hemicellulases, lipases, peroxidases, laccases, α-amylases, glucoamylases, cutinases, pectinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, arabinosidases, mannanases, xyloglucanases, xylanases, pectin acetyl esterases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, other pectate lyases, pectin methylesterases, cellobiohydrolases, transglutaminases; or mixtures thereof.

20. An isolated enzyme having pectate lyase activity, in which the enzyme is (i) free from homologous impurities, and (ii) produced by the method according to claim 17.

21. A detergent composition comprising the enzyme preparation according to claim 18 or the enzyme according to claim 1.

22. A method for improving the properties of cellulosic fibres, yarn, woven or non-woven fabric in which method the fibres, yarn or fabric is treated with an effective amount of the preparation according to claim 15 or an effective amount of the enzyme variant according to claim 1.

23. The method according to claim 22, wherein the enzyme preparation or the enzyme is used in a scouring process step.

24. A method for degradation or modification of plant material in which method the plant material is treated with an effective amount of the preparation according to claim 18 or an effective amount of the enzyme variant according to claim 1.

25. The method according to claim 24 wherein the plant material is recycled waste paper, mechanical paper-making pulps or fibres subjected to a retting process.

26. A variant of a cell-wall degrading enzyme having a beta-helix structure, which variant holds at least one substituent in a position determined by:

(i) Identifying all residues potentially belonging to a stack;

(ii) Characterising the stack as interior or exterior;

(iii) Characterising the stack as polar (typically asparagine, serine, threonine) or hydrophobic (either aliphatic: leucine, isoleucine or valine; or aromatic/heteroaromatic: phenylalanine, tyrosine, histidine, tryptophan) based on the dominating characteristics of the parent or wild-type enzyme stack residues and/or its orientation relative to the beta-helix (interior or exterior);

(iv) Optimising all stack positions of a stack either to hydrophobic aliphatic amino acids, hydrophobic aromatic amino acids (preferably histidine alone, tyrosine and phenylalanine alone or in combination) or polar amino acids (preferably asparagine) by allowing mutations within one or all positions to amino acids belonging to one of these groups;

(v) Measuring thermostability of the variants by DSC or an application-related assay such as a Pad-Steam application test; and

(vi) Selecting the stabilized variants.

27. A method of providing an improved variant of a cell-wall degrading enzyme having a beta-helix structure, the method comprising the steps of:

(i) Identifying all residues potentially belonging to a stack;

(ii) Characterising the stack as interior or exterior;

(iii) Characterising the stack as polar (typically asparagine, serine, threonine) or hydrophobic (either aliphatic: leucine, isoleucine or valine; or aromatic/heteroaromatic: phenylalanine, tyrosine, histidine, and less often

tryptophan) based on the dominating characteristics of the parent or wild-type enzyme stack residues and/or its orientation relative to the beta-helix (interior or exterior);

(iv) Optimising all stack positions of a stack either to hydrophobic aliphatic amino acids, hydrophobic aromatic amino acids (preferably histidine alone, tyrosine and phenylalanine alone or in combination) or polar amino acids (preferably asparagine) by allowing mutations within one or all positions to amino acids belonging to one of these groups;

(v) Measuring thermostability of the variants by DSC or an application-related assay such as a Pad-Steam application test; and

(vi) Selecting the stabilized variants.

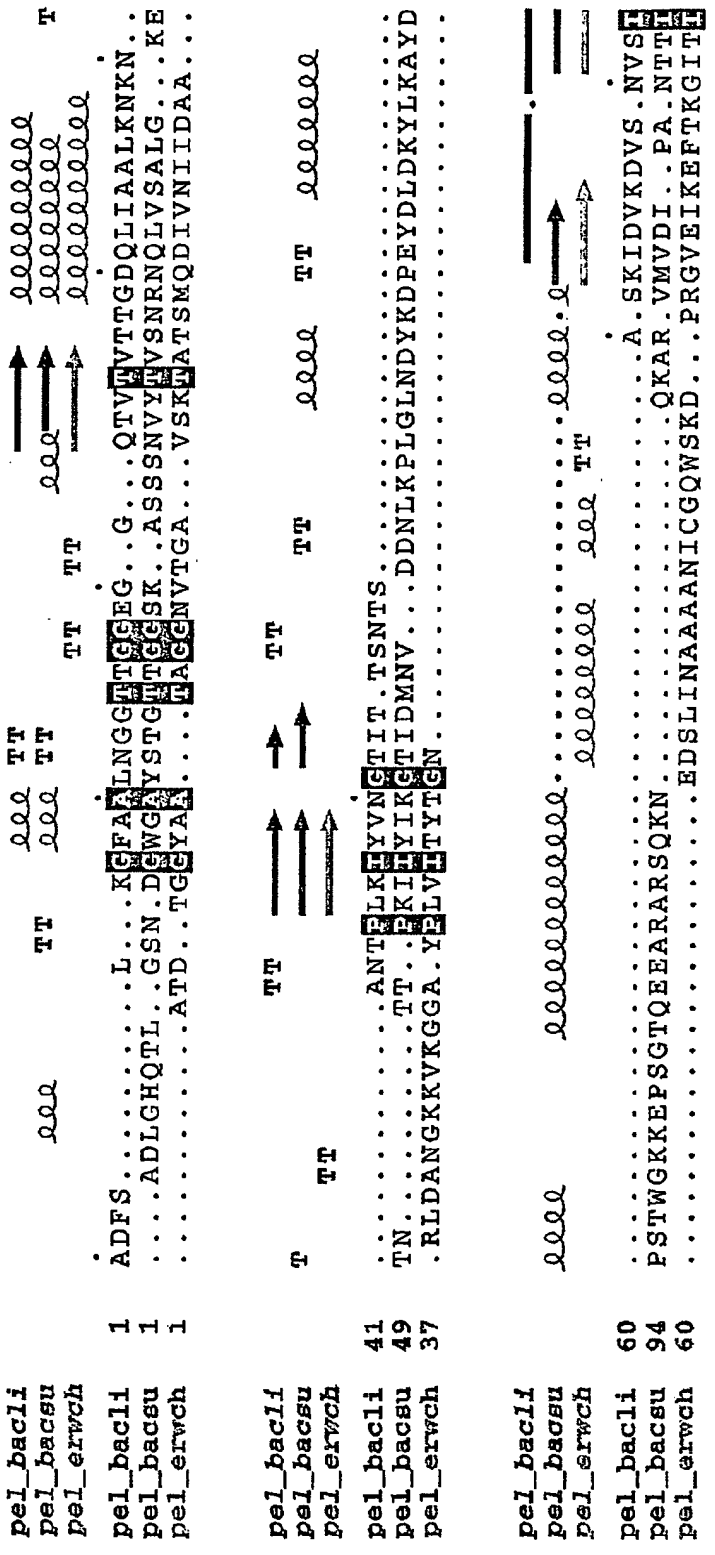
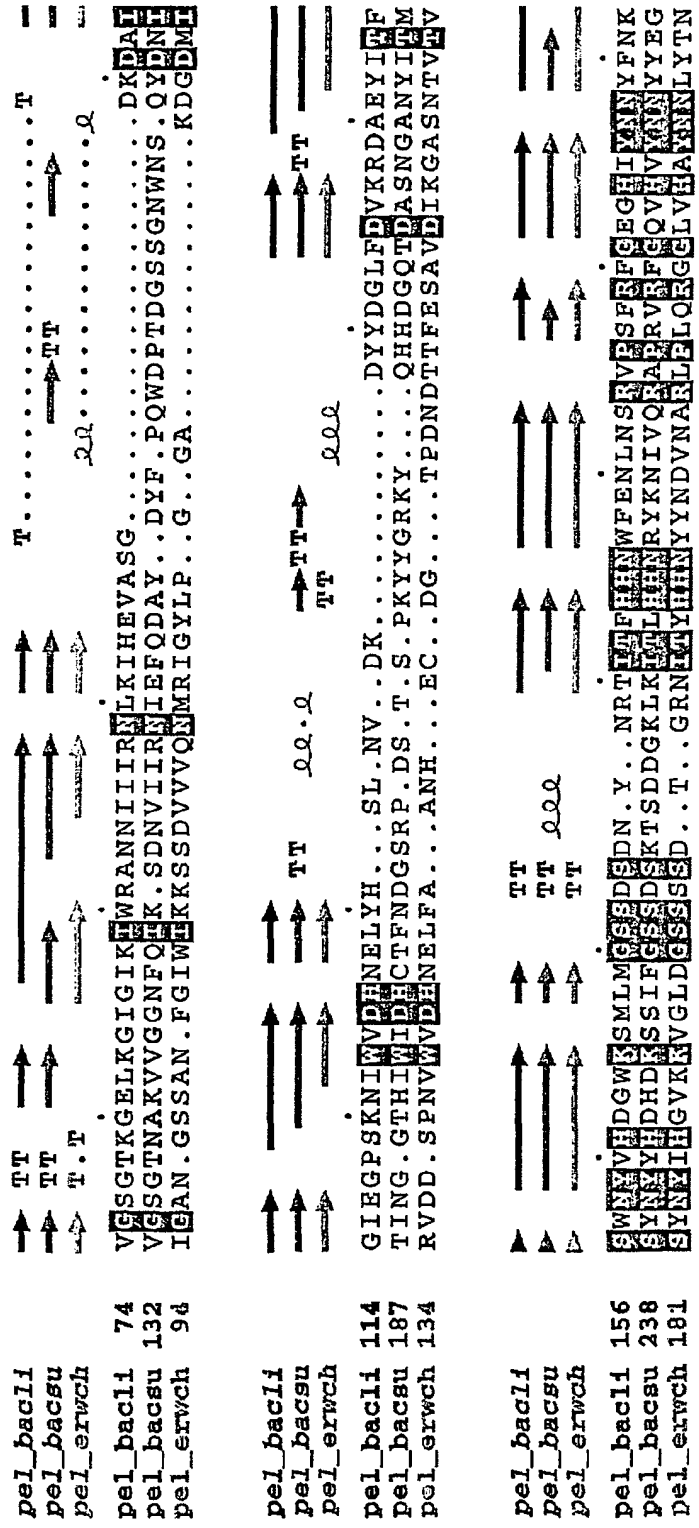


Fig. 1



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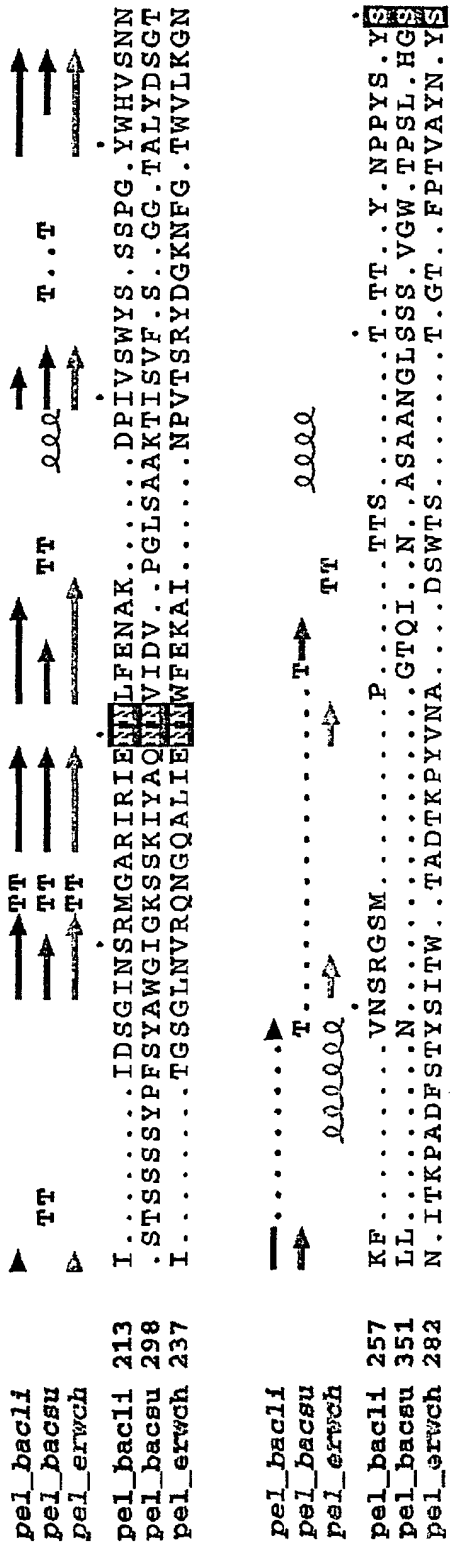

Fig. 1 (continued)

SEQUENCE LISTING

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<130> 10044.204-WO

<160> 18

<170> PatentIn version 3.0

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<211> 909

<212> DNA

<213> Organism: Bacillus licheniformis, ATCC 14580,Enzyme: Pectate lyase, 909 bp, nucleic acid

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gcaaatacgc ctttaaaaat ttatgtcaac ggcaccatta caacatcaaa tacatccgca 180

tcaaagattg acgtcaaaga cgtgtcaaac gtatcgattg tcggatcagg gaccaaaggg 240

gaactcaaag ggatcggcat caaaatatgg cgggccaaca acatcatcat ccgcaacttg 300

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aggatgggcg cgcgcatcag aattgagaac aacctctttg aaaacgccaa agatccgatt 720

gtctcttggt acagcagttc accgggctat tggcatgtat ccaacaacaa atttgtaaac 780

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Gly Gly Glu Gly Gly Gln Thr Val Thr Val Thr Thr Gly Asp Gln Leu
20 25 30

Ile Ala Ala Leu Lys Asn Lys Asn Ala Asn Thr Pro Leu Lys Ile Tyr
35 40 45

Val Asn Gly Thr Ile Thr Thr Ser Asn Thr Ser Ala Ser Lys Ile Asp
50 55 60

Val Lys Asp Val Ser Asn Val Ser Ile Val Gly Ser Gly Thr Lys Gly
65 70 75 80

Glu Leu Lys Gly Ile Gly Ile Lys Ile Trp Arg Ala Asn Asn Ile Ile
85 90 95

Ile Arg Asn Leu Lys Ile His Glu Val Ala Ser Gly Asp Lys Asp Ala
100 105 110

Ile Gly Ile Glu Gly Pro Ser Lys Asn Ile Trp Val Asp His Asn Glu
115 120 125

Leu Tyr His Ser Leu Asn Val Asp Lys Asp Tyr Tyr Asp Gly Leu Phe
130 135 140

Asp Val Lys Arg Asp Ala Glu Tyr Ile Thr Phe Ser Trp Asn Tyr Val
145 150 155 160

His Asp Gly Trp Lys Ser Met Leu Met Gly Ser Ser Asp Ser Asp Asn
165 170 175

Tyr Asn Arg Thr Ile Thr Phe His His Asn Trp Phe Glu Asn Leu Asn

180 185 190

Ser Arg Val Pro Ser Phe Arg Phe Gly Glu Gly His Ile Tyr Asn Asn
195 200 205

Tyr Phe Asn Lys Ile Ile Asp Ser Gly Ile Asn Ser Arg Met Gly Ala
210 215 220

Arg Ile Arg Ile Glu Asn Asn Leu Phe Glu Asn Ala Lys Asp Pro Ile
225 230 235 240

Val Ser Trp Tyr Ser Ser Ser Pro Gly Tyr Trp His Val Ser Asn Asn
245 250 255

Lys Phe Val Asn Ser Arg Gly Ser Met Pro Thr Thr Ser Thr Thr Thr
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Tyr Asn Pro Pro Tyr Ser Tyr Ser Leu Asp Asn Val Asp Asn Val Lys
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Ser Ile Val Lys Gln Asn Ala Gly Val Gly Lys Ile Asn Pro
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<212> PRT

<213> Enzyme: Pectate lyase variant, 302 amino acids, protein

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20 25 30

Ile Ala Ala Leu Lys Asn Lys Asn Ala Asn Thr Pro Leu Lys Ile Tyr
35 40 45

Val Asn Gly Thr Ile Thr Thr Ser Asn Thr Ser Ala Ser Lys Ile Asp
50 55 60

Val Lys Asp Val Ser Asn Val Ser Ile Val Gly Ser Gly Thr Lys Gly
65 70 75 80

Glu Leu Lys Gly Ile Gly Ile Lys Ile Trp Arg Ala Asn Asn Ile Ile
85 90 95

Ile Arg Asn Leu Lys Ile His Glu Val Ala Ser Gly Asp Lys Asp Ala
100 105 110

Ile Gly Ile Glu Gly Pro Ser Lys Asn Ile Trp Val Asp His Asn Glu
115 120 125

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Leu Tyr His Ser Leu Asn Val Asp Lys Asp Tyr Tyr Asp Gly Leu Phe
    130                 135                 140

Asp Val Lys Arg Asp Ala Glu Tyr Ile Thr Phe Ser Trp Asn Tyr Val
145                 150                 155                 160

His Asp Gly Trp Lys Ser Met Leu Ile Gly Ser Ser Asp Ser Asp Asn
                165                 170                 175

Tyr Asn Arg Thr Ile Thr Phe His His Asn Trp Phe Glu Asn Leu Asn
            180                 185                 190

Ser Arg Val Pro Ser Val Arg Phe Gly Glu Gly His Ile Tyr Asn Asn
        195                 200                 205

Tyr Phe Asn Lys Ile Ile Asp Ser Gly Ile Asn Ser Arg Met Gly Ala
    210                 215                 220

Arg Ile Arg Ile Glu Asn Asn Leu Phe Glu Asn Ala Lys Asp Pro Ile
225                 230                 235                 240

Val Ser Trp Tyr Ser Ser Ser Pro Gly Tyr Trp His Val Ser Asn Asn
                245                 250                 255

Lys Phe Val Asn Ser Arg Gly Ser Met Pro Thr Thr Ser Thr Thr Thr
            260                 265                 270

Tyr Asn Pro Pro Tyr Ser Tyr Ser Leu Asp Asn Val Asp Asn Val Lys
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Ser Ile Val Lys Gln Asn Ala Gly Val Gly Lys Ile Asn Pro
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<211> 302

<212> PRT

<213> Enzyme: Pectate lyase variant, 302 amino acids, protein

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Ile Ala Ala Leu Lys Asn Lys Asn Ala Asn Thr Pro Leu Lys Ile Tyr
        35                  40                  45

Val Asn Gly Thr Ile Thr Thr Ser Asn Thr Ser Ala Ser Lys Ile Asp
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Ile Arg Asn Leu Lys Ile His Glu Val Ala Ser Gly Asp Lys Asp Ala
            100                 105                 110

Ile Gly Ile Glu Gly Pro Ser Lys Asn Ile Trp Val Asp His Asn Glu
        115                 120                 125

Leu Tyr His Ser Leu Asn Val Asp Lys Asp Tyr Tyr Asp Gly Leu Phe
    130                 135                 140

Asp Val Lys Arg Asp Ala Glu Tyr Ile Thr Phe Ser Trp Asn Tyr Val
145                 150                 155                 160

His Asp Gly Trp Lys Ser Met Leu Ile Gly Ser Ser Asp Ser Asp Asn
                165                 170                 175

Tyr Asn Arg Thr Ile Thr Phe His His Asn Trp Phe Glu Asn Leu Asn
            180                 185                 190

Ser Arg Val Pro Ser Val Arg Phe Gly Glu Gly His Ile Tyr Asn Asn
        195                 200                 205

Tyr Phe Asn Lys Ile Ile Asp Ser Gly Ile Asn Ser Arg Met Gly Ala
    210                 215                 220

Arg Ile Arg Ile Glu Asn Asn Leu Phe Glu Asn Ala Lys Asp Pro Ile
225                 230                 235                 240

Val Ser Trp Tyr Ser Ser Ser Pro Gly Tyr Trp His Val Ser Asn Asn
                245                 250                 255

Lys Phe Val Asn Ser Arg Gly Ser Met Pro Thr Thr Ser Thr Thr Thr
            260                 265                 270

Tyr Asn Pro Pro Tyr Ser Tyr Ser Leu Asp Asn Val Asp Asn Val Lys
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Ser Ile Val Lys Gln Asn Ala Gly Val Gly Lys Ile Asn Pro
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<213> Bacillus agaradhaerens pectate lyase

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atagataatc gcagccgaag taataaccct gatgaaccat taacgattta tgtaaacgga 180

acgattacac aaggaaattc cccacagtcc cttatagatg ttaaaaatca ccgtggaaaa 240

gctcatgaaa ttaaaaacat ctctattatc ggtgtaggaa caaatggaga gtttgatggc 300

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gtgcgagagg gagaaggcac ggctattgaa gtgacagatg agagtaaaaa cgtgtggatc 420

gatcacaacg agttttatag tgaatttcca ggtaatggag actcagatta ttacgatggt 480

ctcgtagaca taaaaagaaa cgctgaatat attacggttt catggaataa gtttgagaat 540

cattggaaaa cgatgctcgt cggtcatact gataatgcct cattagcgcc agataaaatt 600

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<211> 326

<212> PRT

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<400> 18

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Gly Ala Gly Gly Arg Val Glu Tyr Ala Ser Thr Gly Ala Gln Ile Gln
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Gln Leu Ile Asp Asn Arg Ser Arg Ser Asn Asn Pro Asp Glu Pro Leu
35 40 45

Thr Ile Tyr Val Asn Gly Thr Ile Thr Gln Gly Asn Ser Pro Gln Ser
50 55 60

Leu Ile Asp Val Lys Asn His Arg Gly Lys Ala His Glu Ile Lys Asn
65 70 75 80

Ile Ser Ile Ile Gly Val Gly Thr Asn Gly Glu Phe Asp Gly Ile Gly
85 90 95

Ile Arg Leu Ser Asn Ala His Asn Ile Ile Ile Gln Asn Val Ser Ile
100 105 110

His His Val Arg Glu Gly Glu Gly Thr Ala Ile Glu Val Thr Asp Glu
115 120 125

Ser Lys Asn Val Trp Ile Asp His Asn Glu Phe Tyr Ser Glu Phe Pro
130 135 140

Gly Asn Gly Asp Ser Asp Tyr Tyr Asp Gly Leu Val Asp Ile Lys Arg
145 150 155 160

Asn Ala Glu Tyr Ile Thr Val Ser Trp Asn Lys Phe Glu Asn His Trp
165 170 175

Lys Thr Met Leu Val Gly His Thr Asp Asn Ala Ser Leu Ala Pro Asp
180 185 190

Lys Ile Thr Tyr His His Asn Tyr Phe Asn Asn Leu Asn Ser Arg Val
195 200 205

Pro Leu Ile Arg Tyr Ala Asp Val His Met Phe Asn Asn Tyr Phe Lys
210 215 220

Asp Ile Asn Asp Thr Ala Ile Asn Ser Arg Val Gly Ala Arg Val Phe
225 230 235 240

Val Glu Asn Asn Tyr Phe Asp Asn Val Gly Ser Gly Gln Ala Asp Pro
245 250 255

Thr Thr Gly Phe Ile Lys Gly Pro Val Gly Trp Phe Tyr Gly Ser Pro
260 265 270

Ser Thr Gly Tyr Trp Asn Leu Arg Gly Asn Val Phe Val Asn Thr Pro
275 280 285

Asn Ser His Leu Ser Ser Thr Thr Asn Phe Thr Pro Pro Tyr Ser Tyr
290 295 300

Lys Val Gln Ser Ala Thr Gln Ala Lys Ser Ser Val Glu Gln His Ser
305 310 315 320

Gly Val Gly Val Ile Asn
325